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“Examiner Search Notes”

Thank you.

James Martinell
Primary Examiner 1631

Run on:	November 29, 2003, 17:02:55 ; Search time 106 Seconds (without alignments)	c 28	37.8	2.3	1830121	4	US-09-643-990A-1
Title:	US-09-700-696C-1	c 29	37.6	2.3	1293	4	US-09-700-838-219
Perfect score:	1655	c 30	37.4	2.3	3527	2	US-08-921-994-64
Sequence:	1 gtgaataaagaatataatgttat.....ataaaaaaaaaaaaaaa 1655	c 31	37.2	2.2	1474	3	US-08-921-994-64
Scoring table:	IDENTITY NUC	c 32	36.8	2.2	1038	4	US-09-560-419-4
Gapcost:	Gapext 1.0	c 33	36.8	2.2	2673	4	US-09-533-447A-12
Searched:	569978 seqs, 220691566 residues	c 34	36.4	2.2	1134	4	US-09-528-3017
Total number of hits satisfying chosen parameters:	1139956	c 35	36.4	2.2	4285	4	US-09-510-464-1
Minimum DB seq length: 0		c 36	36.4	2.2	1664976	4	US-08-916-421B-1
Maximum DB seq length: 2000000000		c 37	36.2	2.2	681	4	US-09-534-001C-2725
Post-processing: Minimum Match 0%		c 38	36.2	2.2	870	5	PCT-US9-13658-3
Lassing First 45 summaries		c 39	36.2	2.2	11288	3	US-08-646-301A-1
Database :	Issued_Patents_NA:*	c 40	36.2	2.2	11288	4	US-08-581-968A-4
	1: /cgm2_6/ptodata/1/ina/5A_COMB_seq;*	c 41	36.2	2.2	11288	4	US-08-554-712B-4
	2: /cgm2_6/ptodata/1/ina/5B_COMB_seq;*	c 42	36.2	2.2	15056	4	US-09-474-659-10
	3: /cgm2_6/ptodata/1/ina/6A_COMB_seq;*	c 43	36.2	2.2	30549	4	US-09-534-001C-322
	4: /cgm2_6/ptodata/1/ina/6B_COMB_seq;*	c 44	36.2	2.2	1654976	4	US-08-916-421B-1
	5: /cgm2_6/ptodata/1/ina/6B_PCTUS_COMB_seq;*	c 45	36	2.2	1219	4	US-08-195-705-1
	6: /cgm2_6/ptodata/1/ina/backfile1_seq;*						
ALIGNMENTS							
RESULT 1							
US-08-232-463-14/C							
; Sequence 14, Application US/08232463							
; Patent No. 5670367							
; GENERAL INFORMATION:							
; APPLICANT: DONNER, F.							
; APPLICANT: SCHEIFLINGER, F.							
; APPLICANT: FALKNER, F. G.							
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS							
; NUMBER OF SEQUENCES: 52							
; CORRESPONDENCE ADDRESS:							
; ADDRESSEE: Foley & Lardner							
; STREET: 1800 Diagonal Road, Suite 500							
; CITY: Alexandria							
; STATE: VA							
; COUNTRY: USA							
; ZIP: 22313-0299							
; COMPUTER READABLE FORM:							
; MEDIUM TYPE: Floppy disk							
; COMPUTER: IBM PC compatible							
; OPERATING SYSTEM: PC-DOS/MS-DOS							
; SOFTWARE: PatentIn Release #1.0, Version #1.25							
; CURRENT APPLICATION DATA:							
; APPLICATION NUMBER: US/08/232,463							
; FILING DATE:							
; CLASSIFICATION: 435							
; PRIOR APPLICATION DATA:							
; APPLICATION NUMBER: US/07/935,313							
; FILING DATE:							
; APPLICATION NUMBER: EP 91 114 300.6							
; FILING DATE: 26-AUG-1991							
; ATTORNEY/AGENT INFORMATION:							
; NAME: BENT, Stephen A.							
; REGISTRATION NUMBER: 29,768							
; REFERENCE/DOCKET NUMBER: 304/7/114 IMPU							
; TELECOMMUNICATION INFORMATION:							
; TELEPHONE: (703) 183-9300							
; TELEFAX: (703) 683-4109							
; TELEX: 899149							
; INFORMATION FOR SEQ ID NO: 14:							
; SEQUENCE CHARACTERISTICS:							
; LENGTH: 7218 base pairs							
; TYPE: nucleic acid							
; STRANDEDNESS: single							
; TOPOLOGY: linear							
; IMMEDIATE SOURCE:							
; CLONE: PIZ95c-P1s							
US-08-232-463-14							
Query Match							
4.2%; Score 70; DB 1; Length 7218;							

COUNTRY: USA
 ZIP: 94104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/676,974
 FILING DATE:
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Osman Ph.D., Richard A.
 REGISTRATION NUMBER: 36,627
 REFERENCE/DOCKET NUMBER: UCB96-055
 TELEPHONE: (415) 343-4341
 TELEFAX: (415) 343-4342
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2277 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-676-974-2

Query Match 2.9%; Score 48; DB 1; Length 2277;
 Best Local Similarity 26.1%; Pred. No. 0.0035; Mismatches 119; Indels 3; Gaps 1;
 Matches 205; Conservative 119; Mismatches 458; Indels 3; Gaps 1;

Db 226 AACACCTAGAATGTTCAAACATAATCCAGGAACTGTAATTGCAAGAACAC 285
 Db 214 AARATHAYGNACNGTNGCVAARRARYTINMGAYAARACNARGAARGNAAR 273
 Qy 286 TCGAAGGATAAAAGGAGCTCAAAGGATTCCCAGAAAAGTCAGTAAAGGC 345
 Db 274 AAYGARAAYWNGARTYCNVAARAARGCNAARGCNAARGCNAARGTNGCNGAY 333
 Qy 346 AAAGGACCATGCTGTTAACACATGACTCTCAAAGTCAA 405
 Db 334 AARAARGCMMENYTNTAHTHNGNAAAYTWSNTTYAARTGYWSNGARGAYGAYTNAAR 393
 Qy 406 AAAATCCCAGTGAAGCGGGTTAACAGATTCCTCAAAGAACGGGGCAAT 465
 Db 394 AONGNTTYGONCAPTYYGNGCNGTNYTARGTNAAYAATGCCNAGYGN 453
 Qy 466 GATATATCTCCCTTCAGTGGGACCTTAAAGGACATTCTGGTAAGGAGAA 525
 Db 454 AARATGMGNNTT--YGGNTTYGNCARTTYAARAYTNTYNTBARGGNGNAARGCN 510
 Qy 526 GCTACTGGTCCUTGACCTGAAGCCAAGATATTCAAACAGGGTTTGAGGCCAAGTGA 585
 Db 511 YTNARGNNTAAATGAARSARATHAAARGNMGNACNGTINGCNETINGA 570
 Qy 586 GCTGAGAGTACTCATCTGACCAAAGGCCAGGTATATGAGATCCAGAGAGAA 645
 Db 571 GONAARGAYAATAYAARGAYAANCWNSTGNCNATGARGAARPNENCN 630
 Qy 646 GAAATGTTGAAATACCTGGAACACTGGGATGAAACTGGCAAGGAGATGCTGTT 705
 Db 631 GARNWSNARCAYCARGARWNSTNAARARARGGNGNGARGARGAVATGGARGAR 690
 Qy 706 GATGTCAGCTGTAGGGCAGCAAGGATATCATGGTAGTACCAATTAAAGGGAGCTC 765
 Db 691 GARGARAAYGAYGAGYAGAYGAGYAGGAGGNGNTTYGAYGAYGAR 750
 Qy 766 CCTGGAGAGGAGGAAACAGTGGATGTCGGCAGCAAATGTCACCAAGGGAGGT 825
 Db 751 GAYGARGARGARAYAATGARWNSTAAARGTNAARCCGNTGARATCARBMGN 810
 Qy 826 GAGTTTCATACCTCCCTGACCCCTCAAAGGAAAGGAAAGGCAAGTGTGATGCA 885

Db 811 GCNGITNAARMGNCCNCNCCNGCNAARWSNWSNGAYCAYWSNGARGARGAYWSNGAY 870
 Qy 886 GCTGMAAGTACOAACATAATGAAATTCCTAAAAATGGCAAGGGCTTACCGAGAAGGGT 945
 Db 871 GARGAWSNGAYWSNWAATGAYGAGGNGARGARYTNGCNCARWSNACNWSNACNGAR 930
 Qy 946 GTAGATCATTCTAATGGAAACAGGAAACCTTAATGAAAGAACATGTTCTGTAAG 1005
 Db 931 GARCARGARGAYAARGCNGTNCARGTNWNSNAYAARAAARMGNARYTMCCNWSNGAY 990

RESULT 4
 US-09-098-487-2
 ; Sequence 2, Application US/09098487
 ; Patent No. 5917025
 ; GENERAL INFORMATION:
 ; APPLICANT: COLLINS, Kathleen
 ; TITLE OF INVENTION: Human Telomerase
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; STREET: 268 Bush Street, Suite 1200
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/098,487
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Osman Ph.D., Richard A.
 ; REGISTRATION NUMBER: 36,627
 ; REFERENCE/DOCKET NUMBER: UCB96-055
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415)343-4341
 ; TELEFAX: (415)343-4342
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2277 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; US-09-098-487-2

Query Match 2.9%; Score 48; DB 2; Length 2277;
 Best Local Similarity 26.1%; Pred. No. 0.0035; Mismatches 119; Gaps 1;
 Matches 226 AACACCTAGAATGTTCAAACATAATCCAGGAACTGCAAGAACAC 285
 Db 214 AARATHAYGNACNGTNGCVAARRARYTINMGAYAARACNARGAARGNAAR 273
 Qy 286 TCGAAGGATAAAAGGAGCTCAAAGGATTCCCAGAAAAGTCAGTAAAGGC 345
 Db 274 AAYGARAAYWNGARTYCNVAARAARGCNAARGCNAARGCNAARGTNGCNGAY 333
 Qy 346 AAAGGACCATGCTGTTAACACATGACTCTCAAAGTCAA 405
 Db 334 AARAARGCMMENYTNTAHTHNGNAAAYTWSNTTYAARTGYWSNGARGAYGAYTNAAR 393
 Qy 406 AAAATCCCAGTGAAGCGGGTTAACAGATTCCTCAAAGAACGGGGCAAT 465
 Db 394 AONGNTTYGONCAPTYYGNGCNGTNYTARGTNAAYAATGCCNAGYGN 453
 Qy 466 GATATATCTCCCTTCAGTGGGACCTTAAAGGACATTCTGGTAAGGAGAA 525
 Db 454 AARATGMGNNTT--YGGNTTYGNCARTTYAARAYTNTYNTBARGGNGNAARGCN 510
 Qy 526 GCTACTGGTCCUTGACCTGAAGCCAAGATATTCAAACAGGGTTTGAGGCCAAGTGA 585
 Db 511 YTNARGNNTAAATGAARSARATHAAARGNMGNACNGTINGCNETINGA 570
 Qy 586 GCTGAGAGTACTCATCTGACCAAAGGCCAGGTATATGAGATCCAGAGAGAA 645
 Db 571 GONAARGAYAATAYAARGAYAANCWNSTGNCNATGARGAARPNENCN 630
 Qy 646 GAAATGTTGAAATACCTGGAACACTGGGATGAAACTGGCAAGGAGATGCTGTT 705
 Db 631 GARNWSNARCAYCARGARWNSTNAARARARGGNGNGARGARGAVATGGARGAR 690
 Qy 706 GATGTCAGCTGTAGGGCAGCAAGGATATCATGGTAGTACCAATTAAAGGGAGCTC 765
 Db 691 GARGARAAYGAYGAGYAGAYGAGGNGNTTYGAYGAYGAR 750
 Qy 766 CCTGGAGAGGAGGAAACAGTGGATGTCGGCAGCAAATGTCACCAAGGGAGGT 825
 Db 751 GAYGARGARGARAYAATGARWNSTAAARGTNAARCCGNTGARATCARBMGN 810
 Qy 826 GAGTTTCATACCTCCCTGACCCCTCAAAGGAAAGGAAAGGCAAGTGTGATGCA 885

Db 406 AAAATCCCAGTGTAGGCTGGATGTCAGTCCAGGAACTGCTCAAAGTC 465

QY 757 AAGGAGCTCCTGGAAAGAACAGACTGGATGCTGGCAGCCAAAATGCTCACCA 816
 DB 508 AANGAGGGAAAGATGTAAAGTCAAAGGAGATCAAAGAGACATGSSAAAAGA 567
 QY 817 GGGAGGTTGAGTTCTCATACCTCTGGACCTCAAAGAGAAAGAGAGGAGT 876
 DB 568 GATCAAGGTGAATAGGGAAAGAGCTGGAAAAGAGAAAGTAAAGAGAGGA 627
 QY 877 AGTGATGCCGCTGAAAGTCCAACTATATGAAATTCTTAATG 922
 DB 628 GAAGGAAGAGGAGATGAGATCAAAGAGATGATGGAAAAG 673

RESULT 7

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
 ; DISORDERS, OR DISEASES INVOLVING
 ; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
 ; FILE REFERENCE: 10001-005-999
 ; CURRENT APPLICATION NUMBER: US/09/461,697
 ; CURRENT FILING DATE: 1999-12-14
 ; NUMBER OF SEQ ID NOS: 466
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 191
 ; LENGTH: 699
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-461-697-191

Query Match 2.4%; Score 39.6; DB 3; Length 717;
 Best Local Similarity 43.6%; Pred. No. 0.37; Indels 0; Gaps 0;
 Matches 177; Conservative 0; Mi matches 229;

Qy 517 AAAGGAGAGCTACTGGCTGACCTAGAGGCAAGATATTCAACAGGTTGCGGC 576
 Db 289 AAAGGGAAAGCTGGAAAAGAGCAARGATGAAAGGGAAAGAATGGAT 348
 Qy 577 CCAACTGAACTCTGAGAGTACTCATTTGACACAAAAAGCCAGTTATAATGAGATCCCA 636
 Db 349 AAAATGGAATGAAAGAGATGCAAAAGGAAGATGAAAGAATGAAAGATGAA 408
 Qy 637 GAGAGAGAAATTGTTGAAATACCATTGAAACTTGGAAACTTGGATGAAACTGGCAAGAGGCA 696
 Db 409 GACGGAAAAGCAATTGGAGAGATGAAAGAGAGAGATGAAAAGAGAGAA 468

Qy 697 GATGGTGTGATGTCAGCCUTGAGAGGCAAGATATCGTAGTACCAATT 756
 Db 469 GACACAAAAGAAAACGGAGATGAAAGAAATGAGATGAAAGAGAGGAGATAAA 528
 Qy 757 AAGGAGCTCCCTGGAGAGGAAACAGTGGATGCTGCAGCCAAAATGCTACCAA 816
 Db 529 AAAGGGGAAAGATGTAAGATGAAAGAGATGAAAGAGAGATGAAAGAGAA 588
 Qy 817 GGGAGGTTGAGTTCTCATACCCCTCTGCACCCCTAAAGGAGAGCAGT 876
 Db 589 GATGGAGGTGAAATGGAGAGAAACTGAAAGGAAAGATGAAAGATGAAAG 648
 Qy 877 AGTGTGCACTGAAAGTACCAACTATAATGAAATTCTTAAATG 922
 Db 649 GAAGGAAAAGAGGAGATGAGATGAAAGAGATGTTGAAAAG 694

Query Match 2.4%; Score 39.6; DB 3; Length 699;
 Best Local Similarity 43.6%; Pred. No. 0.37; Indels 0; Gaps 0;

Matches 177; Conservative 0; Mi matches 229;

Qy 517 AAAGGGAAACTGGAAAAGAGCAAAAGTGAATGGAAAGAGATGAAAGAGGAT 330
 Db 577 CCAGTGTGAGTACTCATCTGACACAAAAAGCCAGTTATAATGATCCCA 636
 Db 3331 AAAATGGAATGAAAGGAAAGATGCCAAAAGGAAGAAAGATGCAAAAAGGTGAA 390
 Qy 637 GAGAGAGAAATTGTTGAAATACCATTTGAAACTGGAAAGAGGCA 696
 Db 391 GACGAAAGGAATGGAGAGATGAAAGAGATGAAAGAGAAAGGAAAGA 450
 Qy 697 GATGCTGTGATGTCAGCCTTGTAGAGGCCAACGATATCGGTACTACCAATT 756
 Db 451 GACAAAAAAACAGGAGTTGGAAAAGAGATGAAAGAGAGGATANA 510

Qy 757 AAGGAGCTCCTGGAAAGAACAGACTGGATGCTGGCAGCCAAAATGCTACCAA 816
 Db 511 AAAGGGGAAAGATGAAAGATGAAAGAGATGAAAGAGAGATGAAAAGAA 570

Qy 817 GGGAGGTTGAGTTCTACCTCTGACCCCTAAAGAGAAAGAGAGGAGT 876
 Db 571 GATGAGGTGAAAGGAGAAAGGAGAACTGAAAGGAAAGATTTAAAGAGGAA 630
 Qy 877 AGTGTGCACTGAAAGTACCAACTATAATGAAATTCTTAAATG 922
 Db 631 GAAGGAAAAGAGGAGATGACATCAAAGAGATGATGGAAAAG 676

RESULT 8

US-09-461-697-189
 ; Sequence 189, Application US/09461697

; Patent No. 6277974

; GENERAL INFORMATION:

; APPLICANT: COGNENT NEUROSCIENCE, Inc.

; APPLICANT: Lo, Donald C.

; APPLICANT: Barney, Shawn

; APPLICANT: Thomas, Mary Beth

; APPLICANT: Portbury, Stuart D.

; APPLICANT: Puranam, Kasturi

; APPLICANT: Katz, Lawrence C.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING

; DISORDERS, OR DISEASES INVOLVING

; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING

; FILE REFERENCE: 10001-005-999

; CURRENT APPLICATION NUMBER: US/09/461,697

; CURRENT FILING DATE: 1999-12-14

; NUMBER OF SEQ ID NOS: 466

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 199

; LENGTH: 717

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-09-461-697-189

; FILE REFERENCE: 10001-005-999

; CURRENT APPLICATION NUMBER: US/09/461,697

; CURRENT FILING DATE: 1999-12-14

; NUMBER OF SEQ ID NOS: 466

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 199

; LENGTH: 717

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-09-461-697-189

; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING

; FILE REFERENCE: 10001-005-999

; CURRENT APPLICATION NUMBER: US/09/461,697

; CURRENT FILING DATE: 1999-12-14

; NUMBER OF SEQ ID NOS: 466

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 199

; LENGTH: 717

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-09-461-697-189

TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 187
LENGTH: 774
TYPE: DNA
ORGANISM: Homo sapiens
US-09-461-697-187

Query Match Similarity 2.4%; Score 39.6; DB 3; Length 774;
Best Local Similarity 43.6%; Pred. No. 0.39; Indels 0; Gaps 0;
Matches 177; Conservative 0; Mismatches 229; Indels 0; Gaps 0;

Qy 517 AAAGGAGAAAGGTACTGGTCTGCACCTGAAAGTATTCAACAGGGTTGGAGGC 576
Db 391 AAAGGGAAAGCTGGAAAAGAACAGATGAAAAGGAAAGATGAAAAGGAGAT 450

Qy 577 CCAAGTGAAGTGAGGTACTCATCTGACACAAAGCAGGTATAATGAGATCCA 636
Db 451 AAAATGAAATGAAAGGAGAAGATGCAAAGGAAAGAGATGCAAAGGTGAA 510

Qy 637 GAGAGAGAAAGAAATGGGAAATACCCATTGAACTAGGGATGAAACTGGGAAAGGGCA 696
Db 511 GAGGAAAGGAATGGAAAGATGAAAAGAGAGATGAAAGAGGAGAAAGGAGAA 570

Qy 697 GATGCTTGTGATGTCGCCCTGTAGGGCACCAACGATATGATGGTAGTACCAATT 756
Db 571 GACAGAAAAGAACAGAGTGGAAAGAGATGAAAGGAGGAGATAAA 630

Qy 757 AAGGAGCTCCCTGGAAAGAAAGAGTGGATGCTGGAGCAAAATGCTCACCAA 816
Db 631 AAAGGGAAAGGAAAGATGTAAGTCAGAGATGAAAGATGAAAGAAGAGAA 690

Qy 817 CGAAAGCTTGAGTTTCATTACCTCTGCACCCCTCAAAGAGAAAGGGAGT 876
Db 691 GATGAAGCTGAAATGGGAAATGGGAAAGGAGATGAAAGAGAAGGAGAA 750

Qy 877 AGTGTGAGCTGAAACTACCAACTATATGAAATTCTCAAATG 922
Db 751 GAGGAAAGGAGGAAAGTGGATCAAAGAAGATGTTGAAAAAAG 796

RESULT 11
US-09-461-697-184
; Sequence 184, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
; APPLICANT: COGNENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Puranam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; DISORDERS, OR DISEASES INVOLVING
; TREATMENT CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; CELL DEATH
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/461,697
; CURRENT FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 184
; LENGTH: 1669
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-461-697-184

Query Match Similarity 2.4%; Score 39.6; DB 3; Length 1669;
Best Local Similarity 43.6%; Pred. No. 0.55; Indels 0; Gaps 0;

Qy 517 AAGGAGAAAGGTACTGGTCTGCACCTGAAAGTATTCAACAGGGTTGGAGGC 576
Db 470 AAAGGGAAAGCTGGAAAAGAACAGATGAAAAGGAAAGATGAAAAGGAGAT 529

Qy 577 CCAGTGAAGTGAGGTACTCATCTGACACAAAGCAGGTATAATGAGATCCA 636
Db 530 AAAATGAAATGAAAGGAGAAGATGCAAAGGAAAGAGATGCAAAGGTGAA 589

Qy 637 GAGAGAGAAAGAAATGGGAAATACCCATTGAACTAGGGATGAAACTGGGAAAGGGCA 696
Db 590 GACGGAAAGGAAAGGAGAATGGGAAAGGAGATGAAAAGGAGAGATGAAAAGGAGAA 649

Query Match Similarity 2.4%; Score 39.6; DB 3; Length 819;
Best Local Similarity 43.6%; Pred. No. 0.4; Indels 0; Gaps 0;

Qy 517 AAGGAGAAAGGTACTGGTCTGCACCTGAAAGTATTCAACAGGGTTGGAGGC 576
Db 470 AAAGGGAAAGCTGGAAAAGAACAGATGAAAAGGAAAGATGAAAAGGAGAT 529

Qy 577 CCAGTGAAGTGAGGTACTCATCTGACACAAAGCAGGTATAATGAGATCCA 636
Db 530 AAAATGAAATGAAAGGAGAAGATGCAAAGGAAAGAGATGCAAAGGTGAA 589

Qy 637 GAGAGAGAAAGAAATGGGAAATACCCATTGAACTAGGGATGAAACTGGGAAAGGGCA 696
Db 590 GACGGAAAGGAAAGGAGAATGGGAAAGGAGATGAAAAGGAGAGATGAAAAGGAGAA 649

Qy 697 GATGCTGTGATGTCAGCTTGTAGGGCAGAACGATATCATGGCTAGTACCAATT 756
 Db 650 GACAGAAAAGAAACAGGAGGTGGAAAGAAGTAAGATGGAAAGAGAAGGGATAA 709

Qy 757 AAGGAGCTCCCTCGAAGAGAAACAGAGTCGATGCCAGCCAAAATGCTACCA 816
 Db 710 AAAGAGGGAAAGATGTAAGATCAAAGATGAAAGATGAAAGAGAGATGAAAGA 769

Qy 817 CGGAAGGTTGAGTTTCATTACCTTCACCCCTCAAAAGAGAAAAGAGGAGT 876
 Db 770 GATGAACGTTGAAATGAGCAAGAGCTGGAAAGAGAGAGAGAGAGAGAGA 829

Qy 877 AGTGATGGAGCTGAAAGTACCAACTATAATGAAATTCTAAATG 922
 Db 830 GAAGGAAAGAGGAGAGAGAGATGATGCAANGAGATGAGTGGAAAAAAG 875

RESULT 12 US-08-714-918-11/c
 Sequence 11, Application US/08714918
 Patent No. 6037123

GENERAL INFORMATION:
 APPLICANT: Benton, Bret
 APPLICANT: Lee, Ving J.
 APPLICANT: Malouin, Francois K.
 APPLICANT: Martin, Patrick K.
 APPLICANT: Schmid, Molly B.
 APPLICANT: Sun, Dongui

TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
 NUMBER OF SEQUENCES: 111
 NUMBER OF INVENTIONS: TARGET GENES

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 ZIP: 90071-2066

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/265,315
 FILING DATE: March 9, 1999
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/714,918
 FILING DATE: September 13, 1996
 APPLICATION NUMBER: 424
 FILING DATE: December 22, 1995
 APPLICATION NUMBER: 60/009,102
 FILING DATE: September 15, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE DOCKET NUMBER: 222/005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1610
 TELEFAX: (213) 955-0440

INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 719 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

US-08-714-918-11

Query Match Score 39.2; DB 3; Length 719;
 Best Local Similarity 56.1%; Pred. No. 0.48;
 Matches 74; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

Qy 1489 AATGTTTTAAGCAAAGAAAATCATTACAGATCTATGAAATAGGTAACTATTGATAGG 1548
 Db 378 ACTATGTTCACTACAAATTACATATGCAACTGAATATGCAATTGCTTTG 319

Qy 1549 TGTCACTTAAATATGTTGATGTOACAATGCTCTATGTTGCTCTGTACA 1608
 Db 318 GAGTATAAAAACCATGTGCAAAGACAACTGTCTAAACTTAAATTATGTCAT 259

Qy 1609 CATTGAAATATAA 1620
 Db 258 AGTTGATCAA 247

RESULT 13 US-09-365-315-11/c
 Sequence 11, Application US/09265315
 Patent No. 6187541

GENERAL INFORMATION:
 APPLICANT: Benton, Bret
 APPLICANT: Lee, Ving J.
 APPLICANT: Malouin, Francois K.
 APPLICANT: Martin, Patrick K.
 APPLICANT: Schmid, Molly B.
 APPLICANT: Sun, Dongui

TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
 NUMBER OF SEQUENCES: 111
 NUMBER OF INVENTIONS: ACTIVE ON STAPHYLOCOCCUS AUREUS
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 ZIP: 90071-2066

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/265,315
 FILING DATE: March 9, 1999
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/714,918
 FILING DATE: September 13, 1996
 APPLICATION NUMBER: 60/009,102
 FILING DATE: December 22, 1995
 APPLICATION NUMBER: 60/003,798
 FILING DATE: September 15, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE DOCKET NUMBER: 240/247
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440

INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 719 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

US-09-265-315-11

Query Match Score 39.2; DB 3; Length 719;
 Best Local Similarity 56.1%; Pred. No. 0.48;
 Matches 74; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 1489 AATGTTTAAGCAAAAAAATCATTACAGATCTATGAACTAGTAACTTGGAGTAGG 1548
 Db 378 ACTATGTTICATTCACAAATTAGATTATCGAACTATGAAACTCATATTGCTTGT 319
 QY 1549 TGTGATTAAAATAGTGTGAATGTCAAAATGCCCTCATGTTGCTGTGAGA 1608
 Db 318 GAGTAAAGGACTTGCAAAAACAGCAAGTGTCTAACTTAATTATGTTCACT 259
 QY 1609 CATGAAATAAA 1620
 Db 258 AGTTGAATCAA 247

RESULT 14

US-09-265-315-11/c
 Sequence 11, Application US/09265315
 Patent No. 6187541
 GENERAL INFORMATION:
 APPLICANT: Benton, Bret
 APPLICANT: Lee, Ving J.
 APPLICANT: Malouin, Francois
 APPLICANT: Martin, Patrick K.
 APPLICANT: Schmid, Molly B.
 APPLICANT: Sun, Dongxu
 TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
 TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
 TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
 NUMBER OF SEQUENCES: 111
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/265,315
 FILING DATE: March 9, 1999
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/7114,918
 FILING DATE: September 13, 1996
 APPLICATION NUMBER: 60/009,102
 FILING DATE: December 22, 1995
 APPLICATION NUMBER: 60/003,798
 FILING DATE: September 15, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 240/247
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 719 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-265-315-11

RESULT 15

US-09-266-417-11/c
 Sequence 11, Application US/09266417
 Patent No. 6228388
 GENERAL INFORMATION:
 APPLICANT: Benton, Bret
 APPLICANT: Lee, Ving J.
 APPLICANT: Malouin, Francois
 APPLICANT: Martin, Patrick K.
 APPLICANT: Schmid, Molly B.
 APPLICANT: Sun, Dongxu
 TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
 TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
 NUMBER OF SEQUENCES: TARGET GENES
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/266,417
 FILING DATE: March 9, 1999
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/714,918
 FILING DATE: September 13, 1996
 APPLICATION NUMBER: 60/009,102
 FILING DATE: December 22, 1995
 APPLICATION NUMBER: 60/003,798
 FILING DATE: September 15, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 240/248
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 719 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-266-417-11

Query Match 2.4%; Score 39.2; DB 3; Length 719;
 Best Local Similarity 56.1%; Pred. No. 0.48;
 Matches 74; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

Qy 1489 AATGTTTAAGCAAAAAATCATTACAGATCTATGAAATAGGTAACTTGGTAGCG 1548
Db 378 ACTAAGTTTCAATTTCACAAAATTAATTATGAAACTATGAATACTCATATTGCTTGG 319
Qy 1549 TGTCAATTAAAAATAGTTGCTGAATGTCAACAAATGCCCTCTATGTTGCTCTGTAGA 1608
Db 318 GAGTATAAAAAGCACTTGCAAAAACACAAGTGCTTAAACTTAATTATTCTTCACT 259
Qy 1609 CATGAAATAAA 1620
Db 258 AGTTGAACTCA 247

Search completed: November 29, 2003, 18:15:24
Job time : 110 secs

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OM nucleic - nucleic search, using sw mode!

Run on: November 29, 2003, 18:13:30 ; Search time 535 Seconds (without alignments)

10191.985 Million cell updates/sec

Title: US-09-700-696C-1

Perfect score: 1655

Sequence: 1 gtgataaagaataatagtagat.....aaaaaaaataaaaaaaa 1655

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched: 2190069 seqs, 1647345023 residues

Total number of hits satisfying chosen parameters: 4380138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:^{*}

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15: /cgn2_6/ptodata/2/pubna/us60_new_pub.seq:*
16: /cgn2_6/ptodata/2/pubna/us60_pubcomb.seq:*
17: /cgn2_6/ptodata/2/pubna/us60_pubcomb.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1

US-09-794-422-33

; Sequence 33, Application US/09794422

; Publication No. US20030166339A1

; GENERAL INFORMATION:

; APPLICANT: Brown, Thomas A.

; INVENTOR: De Wet, Jeffrey R.

; APPLICANT: Gowen, Lori C.

; APPLICANT: Haines, Lynn M.

; TITLE OF INVENTION: Mammalian Osteoregulins

; REFERENCE:

; CURRENT APPLICATION NUMBER: US/09/794,422

; CURRENT FILING DATE: 2003-02-27

; PRIOR APPLICATION NUMBER: 60/185,617

; PRIOR FILING DATE: 2000-02-29

; PRIOR APPLICATION NUMBER: 60/234,500

; NUMBER OF SEQ ID NOS: 46

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO: 33

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-794-422-33

Query Match 99.0%; Score 1638; DB 12; Length 1876;

Best Local Similarity 100.0%; Pred. 0; Mismatches 0; Index 0; Gaps 0;

Matches 1638; Conservative 0; Mi matches 0; Index 0; Gaps 0;

QY 2 TGAATTAAGATATGATCTAGTAACAGAGATACTCACATGCCGTGAGATGTCGA 61

DB 239 TGATTAAGAAATAATGATCGTAACAGAGATACTCACATGCCGTGAGATGTCGA 298

Sequence 1603, A

Sequence 1, Appli

Sequence 7, Appli

Sequence 3, Appli

Sequence 11753, A

Sequence 5466, AP

Sequence 1153, A

Sequence 6930, AP

Sequence 831, App

Sequence 2, Appli

Sequence 18039, A

QY 62 TTATCCPAAGTCATCTGGAAATAAGCTTGGATGAGATGCTATCGAAC 121

DB 299 TTATCCPAAGTCATCTGGAAATAAGCTTGGATGAGATGCTATCGAAC 358

QY 122 TACATGACCAAGAAAGAAATGGCCAGCTCTCATGAAATAACATGCAACATAATGG 181

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Qy	182	GGCCAGTGCAGTGGGATTAAACTCTGGGGAAAGAAAACAAAGAAACACCTAGGAATG	241	Db	1499	GTCGCAAGTCAACTGAGAGCGATGCTGACTAGTCACCGAGATCCAGGGTGACA	1558
Db	419	GGCCAGTGCAGTGGGATTAAACTCTGGGGAAAGAAAACAAAGAAACACCTAGGAATG	478	Db	1322	GTCGCAAGACCTCTCACCTGTGAGTTGATGAGGAGGCCACCTGACAGCTGACCAAG	1381
Qy	242	TTCTPAAACATAATCCAGGAAGTATGAAATTGCTAAACACACTCGGAGGATAAAAGA	301	Db	1559	GTCGCAAGACCTCTCACCTGTGAGTTGATGAGGAGGCCACCTGACAGCTGACCAAG	1618
Db	479	TTCTPAAACATAATCCAGGAAGTATGAAATTGCTAAACACACTCGGAGGATAAAAGA	538	Qy	1382	GTCGAGAGGAGGATAGAGTGAAGAACACTGAGCCAAAGATACTGAGCCAGGGAA	1411
Qy	302	AGCCTCAAGAGATTCAGCCAGAAAGTCCAGTAAGAACACCCATCGTA	361	Db	1619	GTCGAGAGGAGGATAGAGTGAAGAACACTGAGCCAAAGATACTGAGCCAGGGAA	1678
Db	539	AGCCTCAAGAGATTCAGCCAGAAAGTCCAGTAAGAACACCCATCGTA	598	Qy	1442	TTTTTGCTPATCTTAATAGTCACAGTAAATTCTATTAAGGCTATAATGTTTAAGC	1501
Qy	362	TTCAACACACATTGACTACTCAAACATCTCTCAAAGTCAAAAAAATCCCAAGTGAAT	421	Db	1679	TTTTTGCTATCTTAATAGTCACAGTCTATGAAATTGCTAACTTGTGTCATTTAAAGC	1718
Db	599	TTCAACACACATTGACTACTCAAACATCTCTCAAAGTCAAAAAAATCCCAAGTGAAT	658	Qy	1502	AAAAAAAATCTTACAGATCTATGAAATTGCTAACTTGTGTCATTTAAAGA	1561
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Db	659	TGAGGGCAGCCGGTTATCAGATCTTCAAGAGGAGGACATGATATCTCTTCA	718	Qy	1562	TAGTGGTGTAACTGTCACATAATGCTTCATGTTGCTCTGAGCATGAAATAAAC	1621
Qy	482	GTGGGACGCCAACCTTTAAGGACATTCTCTGTTAACAGAGAGGCTACTGGTCCTGACC	541	Db	1799	TAGTGGTGTAACTGTCACATAATGCTTCATGTTGCTCTGAGCATGAAATAAAC	1858
Db	719	GTGGGACGCCAACCTTTAAGGACATTCTCTGTTAACAGAGAGCTACTGGTCCTGACC	778	Qy	1622	AATATCTCTGATGATAA	1639
Qy	542	TAGAGGCCAGAATATTCAAACAGGGTTCTAGGCCAACTGAGCTGAGTACTCATC	601	Db	1859	AATATCTCTGATGATAA	1876
Db	779	TAGAGGCCAGAATATTCAAACAGGGTTCTAGGCCAACTGAGCTGAGTACTCATC	838				
Qy	602	TTGACACAAAAAGCCAGGTTATAATGATCCAGAGGAAATATGGTGAATA	661				
Db	839	TTGACACAAAAAGCCAGGTTATAATGATCCAGAGGAAATATGGTGAATA	898				
Qy	662	CCATTTGGAACTTAGGGATGAAACTCGGAAAGGGCAGATGCTGTCATGCTAGCCCTTGAG	721				
Db	899	CCATTTGGAACTTAGGGATGAAACTCGGAAAGGGCAGATGCTGTCATGCTAGCCCTTGAG	958				
Qy	722	AGGGCAGCAGCATGATCATGGTAACTACCAATTAGGAGCTCCTGGAGGAAAGGA	781				
Db	959	AGGGCAGCAGCATGATCATGGTAACTACCAATTAGGAGCTCCTGGAGGAAAGGA	1018				
Qy	782	ACAGAGTGGATGCTGGCAGCAANTGTCACCAAGGGGAGTTGATGTTCACTACCTC	841				
Db	1019	ACAGAGTGGATGCTGGCAGCAAAATGTCACCAAGGGGAGTTGATGTTCACTACCTC	1078				
Qy	842	CTGCACCCCTCAAAAGGAAAGAAAAGGCAAGTGTGACTGAAAGTACCACT	901				
Db	1079	CTGCACCCCTCAAAAGGAAAGAAAAGGCAAGTGTGACTGAAAGTACCACT	1138				
Qy	902	ATAATGAAATTCTCTAAATGGCAAGGGAGTACCAAAAGGCAAGTGTGACTCTAAATA	961				
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Qy	962	GGAAACCAAGGCAACCTTAATGAAATAAGGTTCTCTAGTAAAGGCCAAAGTCAGGCC	1021				
Db	1199	GGAAACCAAGGCAACCTTAATGAAATAAGGTTCTCTAGTAAAGGCCAAAGTCAGGCC	1258				
Qy	1022	TGCCATTCTCCPTCTCGCTGTTGATAATGAAATAAGGAAAGTGGATCCTTAAAG	1081	Qy	2	TGAAATAAGGATATTGATCTAGTAACTGAGAAATACTCAATGCCCTGAGATGTCAA	61
Db	1259	TGCCATTCTCTCTGCTGTTGATAATGAAATAAGGAAAGTGGATCCTTAAAG	1318	Db	332	TGAAATAAGGATATTGATCTAGTAACTGAGAAATACTCAATGCCCTGAGATGTCAA	391
Qy	1082	GCCCCAGTCACTGAGATAATAACACATGGCAAAATCATGGTACCCACAGAC	1141	Qy	62	TTTATCTTAAGTCACACTGGAAATAAGGTTGAGATGTCATGCAACAAAC	121
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Db	1379	AAAATAATTCTPACACGGATAAGGCTATGCCAACAGGAAAGGCTCTGGGTAGACAA	1438	Db	452	TACATGACCAAGAAATAATGGGAGCTCTCATGAAATACTGCAACATAATGG	511
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RESULT 2

US-09-794-422-45

; Sequence 45, Application US/09794422

; Publication No. US2003016639A1

; GENERAL INFORMATION:

; APPLICANT: Brown, Thomas A.

; DE WET, Jeffrey R.

; GOWEN, Lori C.

; HAMES, Lynn M.

; TITLE OF INVENTION: Mammalian Osteoregulins

; FILE REFERENCE: PC10445

; CURRENT APPLICATION NUMBER: US/09/794,422

; PRIOR APPLICATION NUMBER: 2000-02-27

; PRIOR FILING DATE: 2000-02-29

; PRIOR APPLICATION NUMBER: 2000-09-22

; PRIOR FILING DATE: 2000-09-22

; NUMBER OF SEQ ID NOS: 46

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 45

; LENGTH: 1969

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-09-794-422-45

Query Match 99.0%; Score 1638; DB 12; Length 1969;

Best Local Similarity 100.0%; Pre. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 1639; Conservative 0; Gaps 0;

US-09-794-422-45

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Qy	TCTPAAACATTAATCCTCAGCAAGTATGCTAAAGGAACTCGAACGAAATAAAAAGA	301	Db	1652 GTCTGAGAACCTCGTACCTCTGTAGTTGATGTAGAGGAGGCCCTGACAGCTGACCG	1711
Db	TCTPAAACATTAATCCTCAGCAAGTATGCTAAAGGAACTCGAACGAAATAAAAAGA	631	Qy	1382 GTGAAGGAGGAGATAGAGTGGAAACTCGAACGAAATACTGGCTCTGGCAA	1441
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Qy	TTCAGCAAAACATTCAGTCACTTAAACATCCTCAAAAGTCAAAAGTCAAAAGTCA	421	Db	1772 TTTCGCTCTATCTTAAAGTCAGCTATAAACTCTTAAAGGCTTAATGTTTAAAGC	1831
Db	TTCAGCAAAACATTCAGTCACTTAAACATCCTCAAAAGTCAAAAGTCAAAAGTCA	751	Qy	1502 AAAAAGAAATCTTAAAGTCTTAAAGTCTTAAAGTCTTAAAGTCTTAAAGTCTTAAAG	1561
Qy	TTGAAGGCAGGGTTATACTAGATCTCAAGAGGAGCAATGATATACTCCCTTC	481	Db	1832 AAAAAGAAATCTTAAAGTCTTAAAGTCTTAAAGTCTTAAAGTCTTAAAGTCTTAAAG	1891
Db	TTGAAGGCAGGGTTATACTAGATCTCAAGAGGAGCAATGATATACTCCCTTC	811	Qy	1562 TAGTTCGTTGAAATGTCACAAATGCCCTCTATGTTGTTGCTCTGAGCATGAAATAAAC	1621
Qy	GTCGGGACGGCCAACCTTTAAAGGACATTCTCTGGTAAGGGAGAAGCTACTGGT	541	Db	1892 TAGTTCGTTGAAATGTCACAAATGCCCTCTATGTTGTTGCTCTGAGCATGAAATAAAC	1951
Db	GTCGGGACGGCCAACCTTTAAAGGACATTCTCTGGTAAGGGAGAAGCTACTGGT	871	Qy	1622 AATATCTCTCGATGATAA	1639
Qy	TAGAAGGCAAGATATTCAAACAGGGTTGGGCCAACATGGAAGTGAAGTGAAGTAC	601	Db	1952 AATATCTCTCGATGATAA	1969
Db	TAGAAGGCAAGATATTCAAACAGGGTTGGGCCAACATGGAAGTGAAGTGAAGTAC	931			
Qy	TTGACACAAAAAGCCAGGTTATACTAGATCCAGAGGAGCAAGAGAAATGGGAAATA	661		RESULT 3	
Db	TTGACACAAAAAGCCAGGTTATACTAGATCCAGAGGAAATACTGGGAAATA	991		US - 09 - 794 - 422 - 5	
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Qy	CCATTGGAAACTTGGGATGAAACTTGCGAAAGGGCAATGGCGTTGATGTCAGCCCTGTAG	992		; Publication No. US20030166239A1	
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Qy	722 AGGGCCAAACCATATCATGGTACCAATTAGGACTCCCTGGAGGAGGAA	781		; APPLICANT: Brown, Thomas A.	
Db	1052 AGGGCCAAACCATATCATGGTACCAATTAGGACTCCCTGGAGGAGGAA	1111		; APPLICANT: De Wet, Jeffrey R.	
Qy	782 ACAGAGTGGATCTGGCAAAATCTCAACAGGAAGTTGACTTCATTCCCTC	841		; APPLICANT: Gowen, Lori C.	
Db	1112 ACAGAGTGGATCTGGCAAAATCTCAACAGGAAGTTGACTTCATTCCCTC	1171		; APPLICANT: Hames, Lynn M.	
Qy	842 CTGCACCTCTAAAGGAAAGGAAAGGGCAATGTGTCAGCTGAAGTACCAACT	901		; TITLE: Mammalian Osteoregulins	
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Qy	962 GGACCPAGCAACCTTAATGAAAAGAACAGTTCTTAGTAAAGTCAGGCC	1021		; PRIORITY APPLICATION NUMBER: 60/185, 617	
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Qy	1082 GCCCCAGTCATCGAAATACTAGTAACTCGAACGAAATACTGGCTCTGGCAA	1141		; SEQ ID NO: 5	
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Db	1472 AAATAATTCTACCGAAATACTGGTATGCCAACAGGAAGGCTCTGGTAGAAC	1531		; ORGANISM: Homo sapiens	
Qy	1202 CCCATTCAACAGGAGTTAGTCGGTAAAGGGTCAAGGAAAGCTGGTAGAAC	1261		US - 09 - 794 - 422 - 5	
Db	1532 CCCATTCAACAGGAGTTAGTCGGTAAAGGGTCAAGGAAAGCTGGTAGAAC	1591		Query Match 99.0% ; Score 1638; DB 12; Length 2019;	
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Db	1592 GTGGCACTTCAGTGAAGGCAATGGTGGCTTCTGGTAGAAC	1651		Matches 1638; Conservative 0; Mismatches 0;	

Db	775	AGCCCTAAAGGAGATTCCCAAGGCCAGAAAAGTCAGTAAAGCAAAAGCACCAATGTA	834	Qy	1442	TTTTGGCTATCTTAATAGTCACAGTATAAAATTCTATTAAAGCTATAATGTTTTAGC	1501
Qy	362	TTCACACAAAGATTGACTCTAAACATCTCTCAAAGTCAAAAAAATCCCAGTGATT	421	Db	1715	TTTTGGCTATCTTAATAGTCACAGTATAAAATTCTATTAAAGCTATAATGTTTTAGC	1974
Db	835	TTCACACAAAGATTGACTCTAAACATCTCTCAAAGTCAAAAAAATCCCAGTGATT	894	Qy	1502	AAAAAAAATCATTACAGATCPATGAAATAGGTAACATTGGTAGTGTGTCATTAAAAA	1561
Qy	422	TTGAAGCGCGGTTAACAGATCTCTCAAGAGAGGGCAATGATATACTCCPTTC	481	Db	1975	AAAAAAAATCATTACAGATCPATGAAATAGGTAACATTGGTAGTGTGTCATTAAAAA	2034
Db	895	TTGAAGCGCGGTTAACAGATCTCTCAAGAGAGGGCAATGATATACTCCPTTC	954	Qy	1562	TAGTTGGTGAATGTCAGAAATGCTCTAATGTTGTTGCTGTAGCTGACATGAAATAC	1621
Qy	482	GTGGGAGCGCCAACCTTTAGGACATTCTGGTAAGGAGAAAGCTACTGTCCTGAC	541	Db	2035	TAGTTGGTGAATGTCAGAAATGCTCTAATGTTGTTGCTGTAGCTGACATGAAATAC	2094
Db	955	GTGGGAGCGCCAACCTTTAGGACATTCTGGTAAGGAGAAAGCTACTGTCCTGAC	1014	Qy	1622	AAATATCTCGATGATAA	1639
Qy	542	TAGAAGGCAAAAGATAATTCAACAGGGTTGGAGGCCAAAGTGAAAGTGAATCATC	601	Db	2095	AAATATCTCGATGATAA	2112
Db	1015	TAGAAGGCAAAAGATAATTCAACAGGGTTGGAGGCCAAAGTGAAAGTGAATCATC	1074				
Qy	602	TGACACAAAGCCAGGTTATAATGAGATCCAGAGAGAGAAATGGTGGAAATA	661		RESULT 5		
Db	1075	TGACACAAAGCCAGGTTATAATGAGATCCAGAGAGAAATGGTGGAAATA	1134		US-10-311-840-3		
Qy	662	CCATTGGAACTTCTGGAGCCAAACTGCGAAAGGGAGATGCTGAGCTGTTGAG	721		/ Sequence 3, Application US/10311840		
Db	1135	CCATTGGAACTTCTGGAGCCAAACTGCGAAAGGGAGATGCTGAGCTGTTGAG	1194		/ Publication No. US20030175808AI		
Qy	722	ACGGCAGCAACGATATCATGGTAGTACCAATTAAAGGAGCTCCCTGGAAAGAGAA	781		/ GENERAL INFORMATION:		
Db	1195	ACGGCAGCAACGATATCATGGTAGTACCAATTAAAGGAGCTCCCTGGAAAGAGAA	1254		/ APPLICANT: KUROKAWA, Tomofumi		
Qy	782	ACAGAGTCGATGCTGGAGCCAAAATGCTACCAAGGGAAAGTTGAGTTCTACCTC	841		/ APPLICANT: YAMADA, Takao		
Db	1255	ACAGAGTCGATGCTGGAGCCAAAATGCTACCAAGGGAAAGTTGAGTTCTACCTC	1314		/ APPLICANT: MORIMOTO, Shigeto		
Qy	842	CTGCACCCCTAAAGGAAAGAAAGGAGGAGTGTAGTCACTGTGAAGTACCACT	901		/ TITLE OF INVENTION: No. US20030175808A1el Protein and its DNA		
Db	1315	CTGCACCCCTAAAGGAAAGAAAGGAGTGTAGTCACTGTGAAGTACCACT	1374		/ FILE REFERENCE: 2738USP0		
Qy	902	ATAATGAAATTCTAAATGGAAAAGGCAATGACCAAGGGTGTAGATCATTCTAATA	961		/ CURRENT APPLICATION NUMBER: US/10/311-840		
Db	1375	ATAATGAAATTCTAAATGGAAAAGGCAATGACCAAGGGTGTAGATCATTCTAATA	1434		/ PRIORITY FILING DATE: 2002-12-18		
Qy	962	CGAACCAAGAACCTTAAATGAAAAAAAGTTCTCTAAAGGGCAAAAGTCAGGGCC	1021		/ PRIOR APPLICATION NUMBER: PCT/JP01/05263		
Db	1435	CGAACCAAGAACCTTAAATGAAAAGGCAAAAGTCAGGGCC	1494		/ PRIORITY FILING DATE: 2001-06-20		
Qy	1022	TGCCATTCTCTCTCGGGCTGCTGATATGAAATCAAACAAATGTTCTTTAATG	1081		/ PRIORITY APPLICATION NUMBER: JP 2000-191088		
Db	1495	TGCCATTCTCTCTCGGGCTGCTGATATGAAATCAAACAAATGTTCTTTAATG	1554		/ NUMBER OF SEQ ID NOS: 10		
Qy	1082	GCCCCATCTGAGAAATAATAAACATGGCAAGAAATAATCATGACCCAC	1141		/ SEQ ID NO 3		
Db	1555	GCCCCATCTGAGAAATAAACATGGCAAGAAATAATCATGACCCAC	1614		/ LENGTH: 1662		
Qy	1142	AAAATAATTCTACCGATAAGGTTGCTCAAGGGAAAGGCTCTGGGTAGAAC	1201		/ TYPE: DNA		
Db	1615	AAAATAATTCTACCGATAAGGTTGCTCAAGGGAAAGGCTCTGGGTAGAAC	1674		/ ORGANISM: Human		
Qy	1202	CCATTGCAACAGGAGTTTGTGCTGAGGGATGAGTACTGTCATCTGAGATC	1261		/ US-10-311-840-3		
Db	1675	CCATTGCAACAGGAGTTTGTGCTGAGGGATGAGTACTGTCATCTGAGATC	1734				
Qy	1262	GPGGCAGTTCACTGAGGGATGTTGACTAGTCCAGGGGTTCCAGGGGTGACA	1321				
Db	1735	GPGGCAGTTCACTGAGGGATGTTGACTAGTCCAGGGGTTCCAGGGGTGACA	1794				
Qy	1322	GTCTGAAGACCTCTGTCACCTGTCAGTGTAGAGGAGCCACCTGACCTGACCAG	1381				
Db	1795	GTCTGAAGACCTCTGTCACCTGTCAGTGTAGAGGAGCCACCTGACCTGACCAG	1854				
Qy	1382	GTGAAGGAGGATAGAAGGAAAGCTGAGTGTAGAGGAGCCAGAAATCTG	1441				
Db	1855	GTGAAGGAGGATAGAAGGAAAGCTGAGTGTAGAGGAGCCAGAAATCTG	1914				

Qy	4.22	TTGAAAGCGGGTTATACAGATCTTAAGAGAGGGACAATGATAATCTCCCTTCA	4.81
Db	7.14	TTGAGCGGGTTATACAGATCTTAAGAGAGGGACAATGATAATCTCCCTTCA	7.73
Qy	4.82	GTGGGACGGCCAACCTTTAAGGACATTCCRGTAACGGAGAGCTACTGGTCTGACC	5.41
Db	7.74	GTGGGACGGCCAACCTTTAAGGACATTCCRGTAACGGAGAGCTACTGGTCTGACC	8.33
Qy	5.42	TAGAAGGCAAAGATATTCAAACAGGGTTGCAAGGCCAAGTGAAAGCTGAGAGTACTCATC	6.01
Db	8.34	TAGAAGGCAAAGATATTCAAACAGGGTTGCAAGGCCAAGTGAAAGCTGAGAGTACTCATC	8.93
Qy	6.02	TTGACCAAAAAGCAGGTTATAATGATCCAGAGAGGAAATGGTGGAAATA	6.61
Db	8.94	TTGACCAAAAAGCAGGTTATAATGATCCAGAGAGGAAATGGTGGAAATA	9.53
Qy	6.62	CCATGGAACCTAGGGTAAACTGGAAGAGGGAGCTGTGATGTCAGCTTGTAG	7.21
Db	9.54	CCATGGAACCTAGGGTAAACTGGAAGAGGGAGCTGTGATGTCAGCTTGTAG	10.13
Qy	7.22	AGGGCAACGATATCTGGTAGTACCAATTAAAGAGCTCCCTGGAGAGGAA	7.81
Db	10.14	AGGGCAACCATATCTGGTAGTACCAATTAAAGAGCTCCCTGGAGAGGAA	10.73
Qy	7.82	ACAGACTGGATGCTGGCAAAATGCTACCAAGGGAGGTTGAGTTCAATCCCTC	8.41
Db	10.74	ACAGACTGGATGCTGGCAAAATGCTACCAAGGGAGGTTGAGTTCAATCCCTC	11.3
Qy	8.42	CTGCAACCTCAAAAGAAAAAGAGGCAAGCTGAGTCACTGAAAGTACAACCT	9.01
Db	11.34	CTGCAACCTCAAAAGAAAAAGAGGCAAGCTGAGTCACTGAAAGTACAACCT	11.9
Qy	9.02	ATAATGAATTCTAAATGGAAAGGCTAACAGAAAGGTCTGATCTTAATAA	9.61
Db	11.94	ATAATGAATTCTAAATGGAAAGGCTAACAGAAAGGTCTGATCTTAATAA	12.5
Qy	9.62	GGAACCAAGCAACCTTAATGAAACAAAGGTTCCPAGTAAGGCACAAAGTGGGCC	10.21
Db	12.54	GGAACCAAGCAACCTTAATGAAACAAAGGTTCCPAGTAAGGCACAAAGTGGGCC	13.13
Qy	10.22	TGCCCATTCCTCTCGTGTCTGATTAATGAAATAACAAACGAAATGGATTCCPTTAATG	10.81
Db	13.14	TGCCCATTCCTCTCGTGTCTGATTAATGAAATAACAAACGAAATGGATTCCPTTAATG	13.77
Qy	10.82	GCCCCAGCTCATGAGAATAATACACATGGCACAAATAATCATGATGACCCCGAC	11.41
Db	13.74	GCCCCAGCTCATGAGAATAATACACATGGCACAAATAATCATGATGACCCCGAC	14.31
Qy	11.42	AAATAATTCTACCGGATAACGGTATGCCAAGGGAAAGGTTCTGGGTAAACAC	12.01
Db	14.34	AAATAATTCTACCGGATAACGGTATGCCAAGGGAAAGGTTCTGGGTAAACAC	14.91
Qy	12.02	CCCATTCACAGGGGTTAGTCCCTGAGAAGATGACAGTGTGACTCATGTACA	12.61
Db	14.94	CCCATTCACAGGGGTTAGTCCCTGAGAAGATGACAGTGTGACTCATGTACA	15.55
Qy	12.62	GTGGCACTTCAGTGAGCGATGGTACTGTCACCGAGTTCCAGGGGTGACA	13.21
Db	15.54	GTGGCACTTCAGTGAGCGATGGTACTGTCACCGAGTTCCAGGGGTGACA	16.13
Qy	13.22	GTCTGAGACCTCGTACCTGAGTGTGAGAGAGGCCACTGA	13.70
Db	16.14	GTCTGAGACCTCGTACCTGAGTGTGAGAGAGGCCACTGA	16.62

RESULT 6
US-10-311-840-2
; Sequence 2, Application US/10311840
; Publication No. US20030175808A1
; GENERAL INFORMATION:
; APPLICANT: KURCKAWA, Tomofumi
; APPLICANT: YAMADA, Takao
; APPLICANT: MORIMOTO, Shigreto

Db	406	CCGGAGATGCTAATGATGCTTAAGTCTCTTAAGACATAAGGATCAGAGGTAT	4.65
Qy	316	TCCCAGCCGAAAGTCAGTAAAG-----CAAAGGCCCATGTTCAAA	3.66
Db	466	CTGCTAACCCAGAGGCCCGCTCAAAACACACCCGGAGAACCGGA	5.25
Qy	367	CACAACTTGTACTCTAAACATCTCTCAAGTCAAATAATCCCGTATTGAA	4.26
Db	526	CGGAGGACTCACTACCTGACACATCTCCACAGATCAAGAGACTCCAGT	5.85
Qy	427	GCGAGCGTTATAAGACATTCTCTGAAAGCTACTGTCGACCTGAA	4.86
Db	586	GGCGTGGCTCCCGAGATCTAGTGAGGGAGAAATGATGTCCTGAA	6.45
Qy	487	GACGGCCAACCTTTAAGGACATTCTCTGAAAGCTACTGTCGACCTGAA	5.46
Db	646	GATGGGCAACATTCTGGCAATTCTGGCAAAAGG-----AGCTGCTGGCTCTGAA	7.02
Qy	547	GCGAAAGATATTCAACAGGTTGGAGGCCAAGTGAAGGTGAGGTACTCATCTGAC	6.06
Db	703	AGCTCAACTGCGCC--CCTCTTAGGCTCCAGAAAGTGAAGTTATGACCCACAT	7.59
Qy	607	ACAAAAGCCAGGTTATAATGAGATCCCAGAGGAGAAAGAAAATGCTGAAATACATT	6.66
Db	760	ATGAGTGGACTAGGCTTAATGAGATCCGGAGAGACATGCTGGAGATGCTGAA	8.19
Qy	667	GGAACATGGGTGAACTGCGAAAGGGCAGATGCTGTTGATGTCAGCCCTGAGGGC	7.26
Db	820	GCAACCGAGACAACGCTGCACAGGGCAGCGCTCTGCAAGTGGCCCTGCGGGC	8.79
Qy	727	AGCAACGATATCATGGTAGTACCAATTAAAGGACTCTCCCTGAGAGAGGAACAGA	7.86
Db	880	AGCAATGAAATCACAGGGCAGGACCAATTTCAGGGAACTCCGGAAAGGGAAACAGA	9.39
Qy	787	GTTGGATCTGGAGGCCAAATGCTCACCACCGGAACGTTGATGTTTCAAGCTCTGCA	8.46
Db	940	ATTAACTCCGGAGGCCAAATGCTCTCAAGGAAGTGAATTCAAGTGT	9.99
Qy	847	CCCTCAAAAGAAAAAGAAAGCCAGTGTGAAAGTCAACATTAAAT	9.06
Db	1000	GCCTCTGGAGAAAACTTAACGGCCCTGGAGACATGCA---GGGAGCTGGTCAAC	10.56
Qy	907	GAAATTCTTAAATTAACAGGCAACTTACCGAAACGGTGTAGATCTTAATAGGAAC	9.66
Db	1057	GAAATCCCAAGGAGG2GCAAGGTAGCTTAGCAAAAGATGAGAAGTCCAAGGGAAC	11.16
Qy	967	CAAGCAACCTTAATGAAACAAAGTTCTGAGCAAGAAATTCAGGATCTTAAATGCC	10.26
Db	1117	CAATTAACTTGACTCAAGGCAAACTTCAAGGAAATGCTGAAATGAGA-----	11.76
Qy	1027	ATTCCCTCTGGTCTGTATAATGAAATGAAACAAAGAAATGGATTCTTAATGCC	10.86
Db	1177	CTGGCCCTCTGAGCTTAACTGAGCTTAACTGAAAGTCAAGTGA-----	12.14
Qy	1087	AGTCATGAGATAATAACATGCAAGGAAATATCATTATGTCACAGAACAAAT	11.46
Db	1215	- - - - - AGAAAACCATATGTTCCATGGAAATAATGAAATGAAAT	12.45
Qy	1147	AATTCTACAGCGAAATAAGGCTATGCAACAGGAAAGGCTCTGGT---AGCAACCC	12.03
Db	1246	AATCTACACGGATCTACCGGATCTACAGGCAAACTGGGCTGACAGT	13.05
Qy	1204	CATTCCACGGAGSTTGTCCGTAGAGGGATGACAGTAGTGTCACTGCAAGT	12.63
Db	1306	AATTCCACAGGGCTGACCTGAGCTGGTCAACCGCCAAAG-----AGCAACGAGCTGTCAGT	13.62
Qy	1264	GGCAGTCACTAAGTGTGAGGGCTGAGCTGTCACAGGAGGTTCCAGGGGTGACAGT	13.23
Db	1363	GGGAGTCTTGTGAGTCATGGTCACTGCTGGATTGAAACAGT-----	14.11
Qy	1324	CTGAGAACCTCGTCGTCACCTGAGCTGAGCTGAGCTGAACTGAGGT	13.83

Query Match 2.8%; Score 46.8; DB 12; Length 345;
 Best Local Similarity 46.8%; Pred. No. 0.068; Indels 0; Gaps 0;
 Matches 81; Conservative 0; Mismatches 92; Delins 0; Gaps 0;
 Other Information: n = A,T,C or G

Db 200 NTTNNNNNGNNTNNAAAANTTNNNNNTNNAAANNNTTNTTNAGG 141
 Qy 1603 TGTAGACATGAAAATTAACATATCTCGATGATAA 1655
 Db 140 GGCGCAAAATTTTNTNNAAANNNTTNTNNAGG 88

RESULT 13
 US-10-032-585-6930
 ; Sequence 630, Application US/10032585
 ; Publication No. US20030180953A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Terry, Roemer D.
 ; APPLICANT: Bo, Jiang
 ; APPLICANT: Charles, Boone
 ; APPLICANT: Howard, Bussey
 ; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
 ; FILE REFERENCE: 10182-005-999
 ; CURRENT APPLICATION NUMBER: US/10/032,585
 ; CURRENT FILING DATE: 2001-12-20
 ; NUMBER OF SEQ ID NOS: 8000
 ; SEQ ID NO: 6930
 ; LENGTH: 2826
 ; SOFTWARE: PatentIn version 3.1
 ; TYPE: DNA
 ; ORGANISM: Candida albicans
 US-10-032-585-6930

Query Match 2.8%; Score 46.6; DB 12; Length 2826;
 Best Local Similarity 51.2%; Pred. No. 0.28; Indels 0; Gaps 0;
 Matches 109; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

Db 21 TCCTTATAATAATAATAATTCGACATCAAATCAGGGTCTCCCTTCATAAACT 80
 Qy 951 TCATTCTAATAGGAAACCAAGAACCTTAATGAAAACAAAGCTTCTTAGTAAGGGCAA 1010
 Db 21 TCCTTATAATAATAATAATTCGACATCAAATCAGGGTCTCCCTTCATAAACT 80

Qy 1011 AAGTCAGGCGCTGCCCATCCCTCTCGGGCTCTGATAATGAATCAAACGAATGAA 1070
 Db 81 AATATTGCGATTCATTTGGCTGTGTATATGATTTAATTAATGATAAACAA 140

Qy 1071 TTCCCTTAATGGGCCAGTCATAGGAAATAATAACATGGGAGAAATATCATATATG 1130
 Db 141 AACTCATATAAACATACACCTTATATCATACCAATAATTCTGATAATCTCATGATG 200

Qy 1131 ACCCACAGACAAAAATAATTCTACCGGAATA 1163
 Db 201 AACCACTTACAAATAATTCTACCAATAA 233

RESULT 14
 US-09-387-576-831/c
 ; Sequence 831, Application US/09887576
 ; Patent No. US20020144047A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Budworth, P.
 ; APPLICANT: Brown, D.
 ; APPLICANT: Chang, H.
 ; APPLICANT: Zhu, T.
 ; APPLICANT: Han, B.
 ; APPLICANT: Wang, X.
 ; APPLICANT: Cooper, Bref
 ; TITLE OF INVENTION: Promoters for regulation of plant expression
 ; CURRENT APPLICATION NUMBER: US/09/887 576
 ; CURRENT FILING DATE: 2001-06-25
 ; PRIOR APPLICATION NUMBER: US 60/213, 848
 ; PRIOR FILING DATE: 2000-06-23
 ; PRIOR APPLICATION NUMBER: US 60/214, 087
 ; PRIOR FILING DATE: 2000-06-23
 ; PRIOR APPLICATION NUMBER: US 60/258, 692
 ; PRIOR FILING DATE: 2000-12-29
 ; NUMBER OF SEQ ID NOS: 875
 ; SOFTWARE: Fast-SEQ for Windows Version 4.0

Query Match 2.8%; Score 46.8; DB 12; Length 345;
 Best Local Similarity 46.8%; Pred. No. 0.068; Indels 0; Gaps 0;
 Matches 81; Conservative 0; Mismatches 92; Delins 0; Gaps 0;
 Other Information: n = A,T,C or G

Db 1483 GGCTATAATGTTTAAGCAAAATTCATACAGATCTAGAAATAGGAAACATTTG 1542
 Qy 1543 AGTAGGTGTCATTTAAATAAGTGGTCAATGTCACAAATGCCTCTATGTTGCTC 1602

; SEQ ID NO: 831
 ; LENGTH: 2000
 ; TYPE: DNA
 ; ORGANISM: Oryza sativa
 US-09-887-576-831

Query Match 2.8%; Score 45.8; DB 10; Length 2000;
 Best Local Similarity 53.0%; Pred. No. 0.3%;
 Matches 98; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

Qy 1471 AATTCATTAAAGCTTATATGTTTAAGCAAAAAAATCATTACAGCTATGAAAT 1530
 Db 1269 ACTACTGCTGTATCTGTACTGTACCCATACATATTACTCCATCTAAAGA 1210

Qy 1531 AGGTAACATTAGTAGGTGTCATTAAATAAACATAATAGTTGGTAAGTCACAAATGCCTCA 1590
 Db 1209 AAGTAGTTAGGAATATGCCAAATCAATCTTAAATCAATCTTAAATCTTAA 1150

Qy 1591 TGTGTTCTCTGTAGCTGAAATAAACATAATCTCGTGTATAA 1650
 Db 1149 AGTGTGTTGAAATAATAAAATTTATATATGTTGTCCTTGAAATAATT 1090

Qy 1651 AAAA 1655
 Db 1089 TATAA 1085

RESULT 15
 US-10-312-841-2/c
 Sequence 2, Application US/10312841
 Publication No. US20030186277A1.
 GENERAL INFORMATION:
 APPLICANT: Agenomix AG
 TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
 FILE REFERENCE: E01/1208/WO
 CURRENT APPLICATION NUMBER: US/10/312,841
 CURRENT FILING DATE: 2002-12-30
 NUMBER OF SEQ ID NOS: 2
 SEQ ID NO 2
 LENGTH: 3673778

TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
 NAME/KEY: unsure
 LOCATION: (379615)

US-10-312-841-2

Query Match 2.7%; Score 44.8; DB 12; Length 3673778;
 Best Local Similarity 50.5%; Pred. No. 70; Mismatches 107; Indels 0; Gaps 0;

Qy 1440 AATTTTGTATTTTATAGTCAGTAAATTCTATTAAGCTATACTTTAA 1499
 Db 10300117 ATICCTTCATAAATTATACAAATAACACTAAATAAACTAAACAAA 10300058

Qy 1500 GCaaaaaaaaaaATCATTAGAGCTATGAAATAAGCTAACTTGTAGTCATTTAA 1559
 Db 10300057 ATAAAATAAAAATAAAATCTAAACACTCTAAATTCTTAACTTAA 1029998

Qy 1560 AATAGTTGGTAATGTCACAAATGCCCTCTATGTTGCTGTACATCAAATA 1619
 Db 10299997 AATCTAAACTATCTTAAATAATCTTAAATTCTTAAATTTAA 10299938

Qy 1620 ACATATCTCTCCATGATAA 1655
 Db 1029937 ACTAATACATACATATAACTCTAAACTCTAA 1029902

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OM protein - protein search, using sw model1
Run on: November 26, 2003, 15:45:42 ; Search time 21 Seconds
(without alignments)
866.365 Million cell updates/sec

Title: US-09-700-696C-2
Perfect score: 22.9
Sequence: 1 VNKEYSINKENTHGLRMS.....RRDDSSSESDGSSSESDDG 430

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:
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 2: /cn2_6/.ptodata/1/iaa/55_COMBO.pep:
 3: /cn2_6/.ptodata/1/iaa/6A_COMBO.pep:
 4: /cgm2_6/.ptodata/1/iaa/6B_COMBO.pep:
 5: /cgm2_6/.ptodata/1/iaa/BTUS_COMBO.pep:
 6: /cgm2_6/.ptodata/1/iaa/backfiles1.pep:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	140	6.1	772	1	US-09-524-757-12	Sequence 12, Appl
2	135	6.0	1187	1	US-08-559-28	Sequence 28, Appl
3	136	6.0	1187	3	US-08-545-860D-28	Sequence 28, Appl
4	136	6.0	1187	5	PCT-US94-04496-28	Sequence 26, Appl
5	136	6.0	1210	3	US-08-559-26	Sequence 26, Appl
6	136	6.0	1210	3	US-08-545-860D-26	Sequence 26, Appl
7	136	6.0	1210	5	PCT-US94-04496-26	Sequence 26, Appl
8	135.5	5.9	723	1	US-07-814-964-11	Sequence 11, Appl
9	135.5	5.9	723	1	US-08-258-442-11	Sequence 11, Appl
10	135.5	5.9	723	1	US-08-328-809-6	Sequence 6, Appl
11	135.5	5.9	723	4	US-08-866-840-6	Sequence 6, Appl
12	135.5	5.9	723	5	PCT-US92-11107-11	Sequence 11, Appl
13	134.5	5.9	1115	2	US-08-568-459A-2	Sequence 2, Appl
14	134.5	5.9	1115	2	US-08-826B-2	Sequence 2, Appl
15	134.5	5.9	1115	4	US-09-210-288-2	Sequence 2, Appl
16	134.5	5.9	1115	6	5198347-6	Patent No. 51,983,47
17	124.5	5.6	703	3	US-08-910-925-4	Sequence 4, Appl
18	127.5	5.6	1235	1	US-08-118-101A-2	Sequence 2, Appl
19	126.5	5.6	455	5	PCT-US93-07261-13	Sequence 13, Appl
20	126.5	5.6	1663	5	PCT-US93-07261-16	Sequence 16, Appl
21	125.5	5.5	1261	3	US-09-208-742-4	Sequence 4, Appl
22	125.5	5.5	1261	4	US-09-332-295-2	Sequence 2, Appl
23	124.5	5.5	1261	4	US-09-709-979-2	Sequence 2, Appl
24	124.5	5.5	1183	4	US-09-134-001C-3530	Sequence 35, Appl
25	123	5.4	493	3	US-09-999-774A-12	Sequence 12, Appl
26	123	5.4	1177	4	US-09-134-001C-5106	Sequence 51,6, Appl
27	123	5.4	1588	5	PCT-US93-07261-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-08-524-757-12
; Sequence 12, Application US/08524757
; Patent No. 5792654
; GENERAL INFORMATION:
; APPLICANT: Conaway, Ronald C.
; APPLICANT: Conaway, Joan W.
; APPLICANT: Bradsher, John N.
; TITLE OF INVENTION: RNA Polymerase Transcription Factor
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RICHARDS, MEDLOCK & ANDREWS
; STREET: 1201 Elm Street, Suite 4500
; CITY: Dallas
; STATE: TX
; COUNTRY: US
; ZIP: 75270-2197
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/524,757
; FILING DATE: 12-Nov-1994
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/13621
; FILING DATE: 29-Nov-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/160087
; FILING DATE: 30-Nov-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Harre, John A.
; REGISTRATION NUMBER: 37,345
; REFERENCE/DOCKET NUMBER: B35006C1PCP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (214) 939-4500
; TELEFAX: (214) 939-4600
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 772 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-524-757-12

Query Match Score 140; DB 1; Length 772;
Best Local Similarity 20.5%; Prod. No. 0.0014;
Matches 87; Conservative 49; Mismatches 144; Indels 144; Gaps 17;

FILING DATE: 11-DEC-91
 ATTORNEY/AGENT INFORMATION:
 NAME: DeLuca, Mark
 REGISTRATION NUMBER: 33, 229
 REFERENCE/DOCKET NUMBER: TJu-0855
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-3100
 TELEFAX: (215) 568-3439
 INFORMATION FOR SEQ ID NO: 28:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1187 amino acids
 TBFB: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-320-559-28

Query Match 6.0%; Score 136; DB 1; Length 1187;
 Best Local Similarity 20.6%; Pred. No. 0.058;
 Matches 86; Conservative 52; Mismatches 166; Indels 114; Gaps 14;

Qy 92 AKAHSDKDKKPKORDS-----QAQKSPVKSSTHIEQHNNDYDLKHLISKVK 135
 Db 530 SQEHSSESKDPPPKSSKAKRAPPEPHGKRSQCSQPAQQEPQPQTVGTKQPK---K 584

Qy 136 KIPSDIEFGSGTYDLOERGNDNDISPSGDGPQFPKDIP---GKE-----ATGPDL 181
 Db 585 PVKASARAGSRSTSLSQEREPCPLPGSDRQTSKDPKVTKGRPAAASNEPKAVPPSS 644

Qy 182 EGKDIQTGFAGPSAES----THLDTKKKPGY----NEIPEREEENGNTGTRDE 227
 Db 645 EKKKHKSSLPPSKALSGPRAKDNVEDRTEPHFALVPLTESQGPHSGSRTSCRQA 704

Qy 228 TAKEADAVDVSLEVSSNDINGSTNKKELPGREGNEY-----DASSQNAHGGKVE 276
 Db 705 VVVOQEDNSKRKLPLPLRDTXKLSPLSPRDLTTPPQSLMVKITLDDLSRTPQPPGKGSSQRKAE 764

Qy 277 FHYPPAPSKEKRGSSDAEESTNNANEIIPKNGKGSTRGVYDHSNRNQATINEKORFPSKG 336
 Db 765 DKQPAAGKHSSEKERSSDSS---SKLAKKRKKGAEARDCD-----NKKIR---- 805

Qy 337 KSQQLPIPSRLNRDNEIKNEMDSFGNPSHEN-----HGRKYHYPHRQNNTSRNK 388
 Db 806 -----LEKEIKSOSSSSSSHKESSKTKEPSRSPSSQSKEMLPPPPVSSSQKP 854

Qy 389 GMPOQKGS-----WGRQP-----HSNRFSSRRDDSSSSSGSSSE--SDGD 430
 Db 855 AKPALKRSRREADTCQDPPKSASSTKSNHKDSS-1PKQRRVEGKGSRSSEHKGGSGD 912

RESULT 3
 US-08-320-559-28
 Sequence 28, Application US/08320559
 Patent No. 5633135
 GENERAL INFORMATION:
 APPLICANT: Crote, Carlo
 APPLICANT: Canaani, Eli
 TITLE OF INVENTION: Diagnostics, Therapeutics and Methods for
 Detection and Treatment of Acute Leukemias
 TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the
 TITLE OF INVENTION: All-1 Region
 NUMBER OF SEQUENCES: 44
 CORRESPONDENCE ADDRESS:
 STREET: Woodcock Washburn Kurtz Mackiewicz & No. 5633135ris
 CITY: One Liberty Place - 46th Floor
 CITY: Philadelphia
 STATE: PA
 ZIP: 19103
 COMPUTER READABLE FORM:
 MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: WORDPERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/320,559
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/062,443
 FILING DATE: 14 MAY 1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/971,094
 FILING DATE: 30-OCT-92
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/888,830
 FILING DATE: 27 MAY 92
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/805,093

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,860D
FILING DATE: 07-MAR-1996
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04496
FILING DATE: 22-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10930
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/327,392
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/320,559
FILING DATE: 11-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/062,443
FILING DATE: 14-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/971,094
FILING DATE: 30-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/888,839
FILING DATE: 27-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/805,093
FILING DATE: 11-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Deluca Bego, Mark
REGISTRATION NUMBER: 33,229
REFERENCE DOCKET NUMBER: TJJU-1262
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1187 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
-08/545,860D

NAME: DeLuca Esq., Mark
 REGISTRATION NUMBER: 3,229
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-3100
 TELEXFAX: (215) 568-3439
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1210 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-5445-960D-26

Query Match 6.0%; Score 136; DB 3; Length 1210;
 Best Local Similarity 20.6%; Pred. No. 0.059;
 Matches 86; Conservative 52; Mismatches 166; Indels 14; Gaps 14;

Qy 92 AKAHSKDKKKPQRDS-----QAQKSPVKSSTKTHRIQHNDYLKHLISKVK 135
 Db 553 SQHHSSESKDPPPKSSSKAPRAPPEAPHGGKRSQCKSKPAQQEPQRQTYGTQPK-----K 607

Qy 92 AKAHSKDKKKPQRDS-----QAQKSPVKSSTKTHRIQHNDYLKHLISKVK 135
 Db 553 SQHHSSESKDPPPKSSSKAPRAPPEAPHGGKRSQCKSKPAQQEPQRQTYGTQPK-----K 607

Qy 136 KTPSDFEGCGYTDLQERGNDLSPPSGDQGPFKDIP-----GKGB-----
 Db 608 PYKASARAGSRSTSLSQGERGLPYGSRDQTSDKPKVTKGRPRAASNEPKPAVPPSS 667

Qy 182 EKGDIQPGFAGBSEAES-----THLDTKKGPI-----NEIPEREEENGNTIGTRDE 227
 Db 668 EKKKHKSSLPAFSKALSGPEPAKDNEDRTPHFLVPLTESQGPPHSGSGRTSGRQA 727

Qy 228 TAKEADAVDSLVEGNSNDIMGSTNFKELPGREGNRV-----DAGSQNAHQGKVE 276
 Db 728 VVQEDSRKDRLPLPLRDTKLSPLRDTPPQLSLMVKITDLILSRIFQPGRGSRORKAE 787

Qy 277 FHYPPAPSKEKRKEGSSDAEETNYNEBPKNGKGSPRKGVDHNSNRQATLKEKORPSKG 336
 Db 788 DKQPPAGKHKSSBEKRSDDSS-----SKLAKRKGBEAERDCD-----NKKIR---- 828

Qy 337 KSQGLPLPSRGILDNEIKNEMDSFNGPSHENIT-----HGRRKTHYVPHRQNNSTRNK 388
 Db 829 -----LEKEIKQSOSSSSSSHKESSKTKPSPRSSQSKKMLPPPVSSSSQKQ 877

Qy 389 GMPQGKGS-----WGRQP-----HSNRAFSSRRDDSSSESDGSSSE--SDGD 430
 Db 878 AKPALRKSRRREADTCGDPKSAASSTKSNHKDSSIPKQRVEKGGRSSSEBHKGSSGD 935

RESULT 7 PCT-US94-04496-26

Sequence 26, APPLICATION PC/TUSS9404496

GENERAL INFORMATION:
 APPLICANT: Croce, Carlo
 ATTORNEY: Carraani, Eli
 TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
 TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
 TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1
 NUMBER OF SEQUENCES: 86
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewitz &
 STREET: One Liberty Place, 46th floor
 CITY: Philadelphia
 STATE: Pennsylvania
 COUNTRY: USA
 ZIP: 19103

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/04496
 FILING DATE:

CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: DeLuca Esq., Mark
 REGISTRATION NUMBER: 3,229
 REFERENCE DOCKET NUMBER: TUU-1242
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-3100
 TELEXFAX: (215) 568-3439
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1210 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US94-04496-26

Query Match 6.0%; Score 136; DB 5; Length 1210;
 Best Local Similarity 20.6%; Pred. No. 0.059;
 Matches 86; Conservative 52; Mismatches 166; Indels 114; Gaps 14;

Qy 92 AKAHSKDKKKPQRDS-----QAQKSPVKSSTKTHRIQHNDYLKHLISKVK 135
 Db 553 SQHHSSESKDPPPKSSSKAPRAPPEAPHGGKRSQCKSKPAQQEPQRQTYGTQPK-----K 607

Qy 136 KTPSDFEGCGYTDLQERGNDLSPPSGDQGPFKDIP-----GKGB-----
 Db 608 PYKASARAGSRSTSLSQGERGLPYGSRDQTSDKPKVTKGRPRAASNEPKPAVPPSS 667

Qy 182 EGRDIDQPGFAGBSEAES-----THLDTKKGPI-----NEIPEREEENGNTIGTRDE 227
 Db 668 EKKKHKSSLPAFSKALSGPEPAKDNEDRTPHFLVPLTESQGPPHSGSGRTSGRQA 727

Qy 228 TAKEADAVDSLVEGNSNDIMGSTNFKELPGREGNRV-----DAGSQNAHQGKVE 276
 Db 728 VVQEDSRKDRLPLPLRDTKLSPLRDTPPQLSLMVKITDLILSRIFQPGRGSRORKAE 787

Qy 277 FHYPPAPSKEKRKEGSSDAEETNYNEBPKNGKGSPRKGVDHNSNRQATLNEKORPSKG 336
 Db 788 DKQPPAGKHKSSBEKRSDDSS-----SKLAKRKGBEAERDCD-----NKKIR---- 828

Qy 337 KSQGLPLPSRGILDNEIKNEMDSFNGPSHENIT-----HGRRKTHYVPHRQNNSTRNK 388
 Db 829 -----LEKEIKQSOSSSSSSHKESSKTKPSPRSSQSKKMLPPPVSSSSQKQ 877

Qy 389 GMPQGKGS-----WGRQP-----HSNRAFSSRRDDSSSESDGSSSE--SDGD 430
 Db 878 AKPALRKSRRREADTCGDPKSAASSTKSNHKDSSIPKQRVEKGGRSSSEBHKGSSGD 935

RESULT 8 US-07-814-964-11

Sequence 11, Application US/07814964

PATENT NO. 5559047

GENERAL INFORMATION:
 APPLICANT: Donahue, Brian A.
 APPLICANT: Toney, Jeffrey H.
 APPLICANT: Bruhn, Suzanne L.
 APPLICANT: Lippard, Stephen J.
 APPLICANT: Bill, Peter M.
 APPLICANT: Brown, Steven
 APPLICANT: Rellett, Patri
 APPLICANT: Bessigmann, John M.
 APPLICANT: Lippard, Stephen J.
 TITLE OF INVENTION: DNA Structure Specific Recognition
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 STREET: 2 Militia Drive
 CITY: Lexington
 STATE: MA
 COUNTRY: USA
 ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/814,964
 FILING DATE: 19911226
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/539,906
 FILING DATE: 18-JUN-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Granahan, Patricia
 REGISTRATION NUMBER: 32,227
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-861-6240
 TELEFAX: 617-861-9540
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 723 amino acids
 TYPE: AMINO ACID
 TOPOLGY: linear
 MOLECULE TYPE: protein
 ORIGINAL SOURCE:
 ORGANISM: Drosophila melanogaster
 IMMEDIATE SOURCE:
 CLONE: Drosophila SSRP (predicted)
 FEATURE:
 NAME/KEY: Domain
 LOCATION: 458..507
 OTHER INFORMATION: /label= Acidic
 FEATURE:
 NAME/KEY: Domain
 LOCATION: 518..547
 OTHER INFORMATION: /label= Basic I
 FEATURE:
 NAME/KEY: Domain
 LOCATION: 547..620
 OTHER INFORMATION: /label= HMG-box
 FEATURE:
 NAME/KEY: Domain
 LOCATION: 632..649
 OTHER INFORMATION: /label= Basic II
 FEATURE:
 NAME/KEY: Domain
 LOCATION: 657..723
 OTHER INFORMATION: /label= Mixed Charge
 US-07-814-964-11

Query Match 5.9%; Score 135.5; DB 1; Length 723;
 Best Local Similarity 23.2%; Pred. No. 0_0032;
 Matches 81; Conservative 37; Mismatches 114; Indels 117; Gaps 18;

QY 126 DYLK----HLSKYKIPSPFEGSGYTDLQERGNDISPFSGDQOPFKDIPG-KGEATGPD 180
 DB 416 DYTQKUHVSNNGK---DKSSYKVDFGQSD----NNEPDAYLARUKABAREKE 464

QY 181 LEGKDIQTFAGPSEAESTHLDTYYKPGYNEIPEERENGNTGTRDETAKEADAVDSL 240
 DB 465 EDDDD----GPSDEESTDEFK-KPNENESDAEYDSNEVSDD--DSDASG--- 510

QY 241 EGNDIMGSTNFKELPGREGNRVDAQSNAHQGRKVFFYPPAPSKEKRKEGS----- 292
 DB 511 -GGGDSGAKKKKEKKSEKKEKKEKKEKERTK----KPSKKKKDSGPKRATTA 562

QY 293 ---SDAAS----TNYNEIPKGKSTRKGVDHSRNQATLNFKRFFPSKGKSQGL 341
 DB 563 MLWLNDRPESIKRBNPGLKVTETAKKGEBMWKLKDQSKWEAAKDQRY----- 613

QY 342 PIPSRGLDNEIKNEMDSFNGPSHENITIIGRKHYVPHRQNNSTRNKGMPOQKGWSGR- 399

Db 614 -----HDEMNYKPEAGGDSDNEXG--GKSSKKRKT 642
 Qy 400 QPHSNRR-----FSSSR--RDDSSESSDSGSSE-----SDGD 430
 Db 643 EPSPSKKANTSGSGPKSKEYISDDSTSSDDEKNEPAKKSKPBSDGD 691

RESULT 9
 US-08-258-442-11
 Sequence 11, Application US/08258442
 Patent No. 5670621
 GENERAL INFORMATION:
 APPLICANT: Donahue, Brian A.
 APPLICANT: Toney, Jeffrey H.
 APPLICANT: Brunn, Suzanne L.
 APPLICANT: Pill, Pieter M.
 APPLICANT: Brown, Steven
 APPLICANT: Kellelt, Patci
 APPLICANT: Essigmann, John M.
 APPLICANT: Lippard, Stephen J.
 TITLE OF INVENTION: DNA structure Specific Recognition
 TITLE OF INVENTION: Protein and Uses Therefor
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 STREET: 2 Millett Drive
 CITY: Lexington
 STATE: MA
 COUNTRY: USA
 ZIP: 02173
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/258,442
 FILING DATE:
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/539,906
 FILING DATE: 18-JUN-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Granahan, Patricia
 REGISTRATION NUMBER: 32,227
 REFERENCE/DOCKET NUMBER: MIT-478/AAA
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-861-6240
 TELEFAX: 617-861-9540
 INFORMATION FOR SEQ ID NO: 1:
 IMMEDIATE SOURCE:
 CLONE: Drosophila SSRP (predicted)
 SEQUENCE CHARACTERISTICS:
 LENGTH: 723 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ORGANISM: Drosophila melanogaster
 FEATURES:
 NAME/KEY: Domain
 LOCATION: 518..547
 OTHER INFORMATION: /label= Basic I
 NAME/KEY: Domain
 LOCATION: 632..649
 OTHER INFORMATION: /label= Basic II
 NAME/KEY: Domain
 LOCATION: 657..723
 OTHER INFORMATION: /label= Mixed Charge
 US-07-814-964-11

Query Match 5.9%; Score 135.5; DB 1; Length 723;
 Best Local Similarity 23.2%; Pred. No. 0_0032;
 Matches 81; Conservative 37; Mismatches 114; Indels 117; Gaps 18;

QY 126 DYLK----HLSKYKIPSPFEGSGYTDLQERGNDISPFSGDQOPFKDIPG-KGEATGPD 180
 DB 416 DYTQKUHVSNNGK---DKSSYKVDFGQSD----NNEPDAYLARUKABAREKE 464

QY 181 LEGKDIQTFAGPSEAESTHLDTYYKPGYNEIPEERENGNTGTRDETAKEADAVDSL 240
 DB 465 EDDDD----GPSDEESTDEFK-KPNENESDAEYDSNEVSDD--DSDASG--- 510

QY 241 EGNDIMGSTNFKELPGREGNRVDAQSNAHQGRKVFFYPPAPSKEKRKEGS----- 292
 DB 511 -GGGDSGAKKKKEKKSEKKEKKEKERTK----KPSKKKKDSGPKRATTA 562

QY 293 ---SDAAS----TNYNEIPKGKSTRKGVDHSRNQATLNFKRFFPSKGKSQGL 341
 DB 563 MLWLNDRPESIKRBNPGLKVTETAKKGEBMWKLKDQSKWEAAKDQRY----- 613

QY 342 PIPSRGLDNEIKNEMDSFNGPSHENITIIGRKHYVPHRQNNSTRNKGMPOQKGWSGR- 399

APPLICANT: Toney, Jeffrey H. 465 BDDDD ---- GDSSBESTDDBF - KPNENSVDVAEYDSNVSDDD -- DSDASG---- 51
 APPLICANT: Bruhn, Suzanne L. 241 EGNSNDIMGSTNFKEPLPGREGNRVDAQSGONAHOGKTEFHYPAPSSKEKRKEGS----- 292
 APPLICANT: Pil, Pieter M. 511 -GGNSDGAKKKKEKSEKEKEKKERKTK----- KPSKSKKDSCGPKRATTAFAF 562
 APPLICANT: Brown, Steven
 APPLICANT: Kelley, Patti
 TITLE OF INVENTION: Uses for DNA Structure-Specific
 NUMBER OF SEQUENCES: 8
 NUMBER OF SEQUENCES: 8
 ADDRESS: Patent Administrator, Testa, Hurwitz & Thibault
 STREET: 53 State Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/866, 840
 FILING DATE: 02-JUN-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Fenton, Gillian M.
 REGISTRATION NUMBER: 36,508
 REFERENCE/DOCKET NUMBER: MIT-023 (5473/24)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-248-7600
 TELEFAX: 617-248-7100
 SEQUENCE CHARACTERISTICS:
 LENGTH: 723 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ORIGINAL SOURCE:
 ORGANISM: *Drosophila melanogaster*
 IMMEDIATE SOURCE:
 CLONE: *Drosophila SSRP* (predicted)
 FEATURE:
 NAME/KEY: Domain
 LOCATION: 458..507 /label= Acidic
 OTHER INFORMATION:
 FEATURE:
 NAME/KEY: Domain
 LOCATION: 518..547
 OTHER INFORMATION: /label= Basic I
 FEATURE:
 NAME/KEY: Domain
 LOCATION: 547..620
 OTHER INFORMATION: /label= HMG
 FEATURE:
 NAME/KEY: Domain
 LOCATION: 657..723
 OTHER INFORMATION: /label= Mixed Charge
 US-08-866-840-6
 Query Match 5.9%; Score 135.5; DB 4; Length 723;
 Best Local Similarity 23.2%; Pred. No. 0.0032;
 Matches 81; Conservative 37; Nismatches 114; Indels 117; Gaps 18;
 126 DYLK---HLSKVKKPSDFEGSGTYDQRGNDIDSPSGDGFOPKDDPG-KGEATGPD 180
 Qy 416 DYITOKKLHYSNMGR---DKSGYKDV-DFGDSD----NENEYDAYLARKEAREEE 464
 Db 181 LEGKDIQTGAGPSAESTHLDTKPGYNWIPERBENGONTIGDRETAKEADAVDVLV 240
 Qy

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OTHER INFORMATION: /label= Acidic
FEATURE: NAME/KEY: Domain
LOCATION: 518..547
OTHER INFORMATION: /label= Basic I
FEATURE: NAME/KEY: Domain
LOCATION: 547..620
OTHER INFORMATION: /label= HMG_box
FEATURE: NAME/KEY: Domain
LOCATION: 632..649
OTHER INFORMATION: /label= Basic II
FEATURE: NAME/KEY: Domain
LOCATION: 657..723
OTHER INFORMATION: /label= Mixed charge
PCT-US92-111 07-11

Query Match Score 135.; DB 5; Length 723;
Best Local Similarity 23.2%; Pred. No. 0.0032;
Matches 81; Conservative 37; Mismatches 114; Indels 117; Gaps 18;
Qy 126 DYLK---HLSKYKKIPSPREGSXYTDLQERGNDNISPFGDQPFKDIPG-KGRATGPD 180
Db 416 DYITQKKLHVSNNGK----DKSYKXDV-DFGDSD----NENE DAYLARLKAFAREKE 464
Qy 181 LEGKDIQNGFAGPSSEAESTHLDTKPGYNYBIPEREEGGNTIGRDETAKEADAVDSL 240
Db 465 EDDDD----GDSDEETDDEDF KPNNNEESDVAEYDSNVESSDD---DSDASG---- 510
Qy 241 EGSDNDIMGSTNFKEPLGPREGNRVDAGSQNAHQGVYEFHYPPAPSXKEKRGQS---- 292
Db 511 -GGGDSGAKKCKKEKKSKKEKKHEKERT-----KPSKKKROSGGPKRATAF 562
Qy 293 ----SDAEE-----TNYNELPKGNGKSTRKGVDHNSRNOATLNKEKORFPSKGKSQGL 341
Db 563 MLWLNDDRESIKRNPNGKIVTEAKKGEMMWKELKDKSWEDAIAKDQRY----- 613
Qy 342 PIPSRGDNEITKNEMDSSNGPSPHENIITHGRKYHYPHQRNNSTRNKGMDQKGWSGR-- 399
Db 614 -----DNEKMDSSNGPSPHENIITHGRKYHYPHQRNNSTRNKGMDQKGWSGR-- 642
Qy 400 QPHSNRR-----FSSRR----RDDSSESSSDSGSSSE-----SDGD 430
Db 643 EPSPSKRKANTSGSGFKSKKEYISDDSTSSDDEKDNEPAKKSKPSDGD 691

RESULT 13
US 08-568-459A-2
Sequence 2, Application US/08568459A
Patent No. 5849306
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellens, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESS: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

```

SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/568,459A
 FILING DATE: 07-DEC-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Israelsen, Ned
 REGISTRATION NUMBER: 29, 655
 REFERENCE/DOCKET NUMBER: NIH121.001CP1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 235-8550
 TELEFAX: (619) 235-0176
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1115 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: Plasmodium vivax
 8-568-459A-2

Very Match 1st Local Similarity Itches	5.9%; Score 134.5; DB 2; Length 1115; 20.0%; Pred. No. 0.0071; Missmatches 220; Indels 89; Gaps 21;

2 NKEYSISNKENTINGLMSIYKPKSTGNKGPEGDDAIKSLHDQEYGAALIRNMQHIMG 61	
500 NKFTSVKNAEKVQTAGIVTPY-----DILRQ--ELDEFNEVAFENELNRKDG 544	
62 PVTIAKLIG-EENKENTPRVNLIIPASMYNAKAHKKKPORDSQOKSPVKSSTHR 120	
545 AYIELCVCSVEEAKKNTQEVVTVNDAAKSOA-TNSNPTISQPVDSKAEKVP--GDSTH 600	
121 IQRNDYKRLSKV-KKTPSDFEGSGTIDLQ--ERGNDDISPFGDQFDPGKGB- 175	
601 -GRNVNSGODSSSTTGKAVTGDGNGNQTPAESDVQRSDIAESYSARNDVQPKSVRSRSD 658	
176 ---ATGPDLLEGDKITQTFAGPSRAESTHLDTKKPG-----YNEBI 211	
659 TASVYGLIAEAGKE-NLGASNRSRESEY-VEANSPPDDTVNASIIPVYSGENPLVTPYNGL 716	
212 PEREENGPN-----TIGTRDTAKEADAVDVSILEGVNSNDIMGSTNFKEBLPREGRN 261	
717 RHEKDNSDGPASEMANPDNSNSKGEIKGQONDMAKATKDSSNSDGTS---SATGD 771	
262 RVDAGSONAHOGKVEHYHPPAPSKEKKEKGSS--DAARESTNYNEIPKNGKGST--RKG 315	
772 TTDVDRPIKGVPEDRDKTVSSKDGGEEDNSANKDAATVVGEDRIRENSAGSTNDRSK 831	
316 VDHNSRNQDATLNKQR--FPSKGKSQLPIPSRG-LDNEIKNEMDSFNGPSHENITHG 371	
832 NDTEKNGASTPDSKQSEDATALSKTBSLESTBSGDRTTNDTNSLENKNGGEKDLQXHD 891	
372 RKHYHYPHRQNSTR-----NKGKMPQGKCSWGRQPHSNR-RFSSRRDDSESSSDSG 422	
892 FKSNDTPEEPNSDQTTDAEGHDRDS1KNDKAE--RKHMNDTFTKNTNSHLSNNNL 949	
423 SSESBD 428	
950 SNGKLD 955	

APPLICANT: Peterson, David S.
 APPLICANT: Su, Xin-zhuan
 APPLICANT: Wellens, Thomas E.
 TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX NUMBER OF SEQUENCES: 45
 TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS CORRESPONDENCE ADDRESS:
 ADDRESSEE: Knobbe Martens Olson & Bear
 STREET: 620 Newport Center Drive 16th Floor
 CITY: Newport Beach
 STATE: California
 COUNTRY: US
 ZIP: 92660
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/487,826B
 FILING DATE: 10-SEP-1993
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Israelson, Ned
 REGISTRATION NUMBER: 29,655
 REFERENCE DOCKET NUMBER: NIH121.001CP1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 235-8550
 TELEFAX: (619) 235-0176
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1115 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: Plasmodium vivax
 US-08-487-826B-2

Query Match		Best Local Similarity		Score 134,5;		DB 2;		Length 1115;	
	Matches	20.0%	Pred. No.	0.0071;	Mismatches	220;	Indels	89;	Gaps 21;
Qy	2	NKGYISNKENTHNGLRLSTYPKSTGNKGFDGDDAIKSGLHDQEYGAALLRNNMQHIMG	61						
Db	500	NKFISVAKRQVQTAGIVTPY-----	544						
Qy	62	PVTAIKLIG-EENKENTPRVNLTIPASMMNYAKHSKCKPORDSQAQSKPVKSXSKSTHR	120						
Db	545	AIVTELCVSVEAKAKNTQEVVTNDNAKSQA-TMSNPISPVDSKRAVKVP--GDSTH-	600						
Qy	121	IQHNIDYKLHSKV-KKIPSDFFEGSGTYDLQ--	175						
Db	601	--GVNVNSGDSSTSITGKAVTGDGONGNQTPAESVRSQDIAESVAKNVDQPSKSRSSD	658						
Qy	176	--ATGPGLEKGDIQTGFAGCSEAESTHLDTKPG-----	211						
Db	659	TASVTFGIAEAK-NIGAANSRSPBSST-----	716						
Qy	212	PEREEENG---TIGTDETAKADAVDSLVEGSNDIMGSTNFKELPGRGN	261						
Db	717	RHSKDNDSSDGPASESMANPDNSKG>GQDNDMAKATDSSSSDGTG-----SATGD	771						
Qy	262	RUDAGSONAHQKGKVEFHYPAPSKEKRKEGSS--	315						
Db	772	TTDAVDRELINKGVPEDRDKTGSKDGGEDNSANKDAUTVGDRRENSAGGSTNDRSK	831						
Qy	316	VDEHSNMRNQATLNKEQR--EPSKGKSQLPLPSRG--LDNBTKNEMDSFNGPSHENLITHG	371						
Db	832	NDTEKNGASTPDSQSEDATAKSMEESTESTESGRTINDTINSLENTRG3KEULQHQD	891						

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Qy 176 --ATGPDLEGKDIOTGFAGPSEAESTHLDTRKPG----- YNEI 211
Db 659 TASVIGAEGAGE-NLGASNSPSEST-VEANSPGDTVANSASIPIVYGGENLVTPINGL 716
Qy 212 PEREENGNN-----TIGRDETAKEADAVDVSLEVGSENDINGSTMNFELPGREGN 261
Db 717 RHKSDNDSDGPAESMANPDNSNSKGGETKGQONDMAKATKDSSNSDCTS----SATGD 771
Qy 262 RVDAGSONNAHQKVKUEPHYPAPSKERKKGSS--DAEESTINYNEIPKNGKST-- RKG 315
Db 772 TTDADVDRINKSVPEDRDKTVSSKGCGEDNSANKDAATVVGEBDRIRENSAGGSTNDRSK 831
Qy 316 VDHSNRNQATUNBKRQ - FPSKGKSQGLPIPBRG--LDNEBKNMDSFNGPSHENITHG 371
Db 832 NDTEKNGASTPSKQSEDATANSKTESLESTSGDRITNDTINSLENKGKGERDLOKHID 891
Qy 372 RKXHYVPHRONNSTR-----NKGMFQGRGSWGRPHSNR-RFSSRRDSDSSESSDSG 422
Qy 892 FKSNDTPNEEPNSDQTTDAEGHDRTS1KNDKAE - RRKHMNDFTKNTNSHHLNSNNNL 949
Qy 423 SSSESD 428
Db 950 SNGKLD 955

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Search completed: November 26, 2003, 15:49:09
 Job time : 23 secs

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OM protein - protein search, using sw model

Run on: November 26, 2003, 15:48:08 ; Search time 37 Seconds
(without alignments)

Scoring table: BLOSUM62

Title: US-09-700-696C-2

Perfect score: 2279

Sequence: 1 VNKEYSINKENTHNLRLMS.....RRDDSSSDGSSSESDG 430

Total number of hits satisfying chosen parameters: 673684

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:
 1: /cgn2_6/podata/2/pubbaa/US07_PUBCOMB.pep:
 2: /cgn2_6/podata/2/pubbaa/PCT_NEW_PUB.pep:
 3: /cgn2_6/podata/2/pubbaa/US06_PUB.pep:
 4: /cgn2_6/podata/2/pubbaa/US05_PUBCOMB.pep:
 5: /cgn2_6/podata/2/pubbaa/US05_NEW_PUB.pep:
 6: /cgn2_6/podata/2/pubbaa/US04_PUBCOMB.pep:
 7: /cgn2_6/podata/2/pubbaa/US08_NEW_PUB.pep:
 8: /cgn2_6/podata/2/pubbaa/US08_PUBCOMB.pep:
 9: /cgn2_6/podata/2/pubbaa/US09_PUBCOMB.pep:
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 13: /cgn2_6/podata/2/pubbaa/US10_PUBCOMB.pep:
 14: /cgn2_6/podata/2/pubbaa/US10B_PUBCOMB.pep:
 15: /cgn2_6/podata/2/pubbaa/US10C_PUBCOMB.pep:
 16: /cgn2_6/podata/2/pubbaa/US10_NEW_PUB.pep:
 17: /cgn2_6/podata/2/pubbaa/US60_NEW_PUB.pep:
 18: /cgn2_6/podata/2/pubbaa/US60_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2276	99.9	509	12	US-09-794-422-34
2	2276	99.9	525	12	US-09-794-422-6
3	2276	99.9	525	12	US-09-311-840-1
4	2276	99.9	540	12	US-09-794-422-46
5	2276	99.9	556	12	US-09-794-422-8
6	2269	99.6	525	10	US-09-814-550-2
7	983.5	43.2	441	12	US-09-794-422-4
8	938	41.2	435	12	US-09-794-422-2
9	514	22.6	97	10	US-09-812-485A-1
10	246	10.8	47	10	US-09-812-485A-2
11	235.5	10.3	47	10	US-09-812-485A-3
12	229	10.0	47	10	US-09-812-485A-4
13	218	9.6	40	10	US-09-812-485A-23
14	216	9.5	44	10	US-09-812-485A-6
15	215	9.4	44	10	US-09-812-485A-5

ALIGNMENTS

RESULT 1
 US-09-794-422-34 ; Sequence 34, Application US/09794422
 ; Publication No. US20030166239A1 ; GENERAL INFORMATION:
 ; APPLICANT: Brown, Thomas A.
 ; De Wet, Jeffrey R.
 ; Gowen, Lori C.
 ; Haines, Lynn M.
 ; TITLE OF INVENTION: Mammalian Osteoregulins ;
 ; TYPE REFERENCE: PCT/US04/045 ; CURRENT APPLICATION NUMBER: US/09/794,422
 ; CURRENT FILING DATE: 2001-02-27 ; PRED. NO. 4.3e-173;
 ; PRIOR APPLICATION NUMBER: 60/185,617 ; BEST LOCAL SIMILARITY 99.8%;
 ; PRIOR FILING DATE: 2000-02-29 ; MATCHES 429; CONSERVATIVE 1; MISMATCHES 0;
 ; NUMBER OF SEQ ID NOS: 46 ; INDELS 0; GAPS 0;
 ; SOFTWARE: PatentIn Ver. 2.0 ; SEQ ID NO 34
 ; LENGTH: 509 ; ORGANISM: Homo sapiens ;
 ; TYPE: PRT ; SEQ ID NO 34

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2276	99.9	509	12	Sequence 34, Appl
2	2276	99.9	525	12	Sequence 6, Appl
3	2276	99.9	525	12	Sequence 1, Appl
4	2276	99.9	540	12	Sequence 46, Appl
5	2276	99.9	556	12	Sequence 8, Appl
6	2269	99.6	525	10	Sequence 2, Appl
7	983.5	43.2	441	12	Sequence 4, Appl
8	938	41.2	435	12	Sequence 2, Appl
9	514	22.6	97	10	Sequence 1, Appl
10	246	10.8	47	10	Sequence 2, Appl
11	235.5	10.3	47	10	Sequence 4, Appl
12	229	10.0	47	10	Sequence 3, Appl
13	218	9.6	40	10	Sequence 23, Appl
14	216	9.5	44	10	Sequence 6, Appl
15	215	9.4	44	10	Sequence 5, Appl

Db 200 IQHNDYLKHLVKVKIPSEFGSGYTDLQERGNDISPGDGQPPKD1PGKBEATGPD 259
 Qy 181 LEGDIQTGPSEASLTHLDTKKGYNEI PEREENGNTIGTDETAKEADAVDVLV 240
 Db 260 LEGDIQTGPSEASLTHLDTKKGYNEI PEREENGNTIGTDETAKEADAVDVLV 319
 Qy 241 EGSNDIMGSTNFKELPGREGNRVDAAGSQQPKSKQSGLPIPSRGDNEIKNEMDSFN 300
 Db 320 EGSNDIMGSTNFKELPGREGNRVDAAGSQQPKSKQSGLPIPSRGDNEIKNEMDSFN 379
 Qy 301 YNEIPKNGKGSTRKGYDHNSRNQATLNKEQRFPSCKSKQSGLPIPSRGDNEIKNEMDSFN 360
 Db 380 YNEIPKNGKGSTRKGYDHNSRNQATLNKEQRFPSCKSKQSGLPIPSRGDNEIKNEMDSFN 439
 Qy 361 GPSHENITTHGRKYHYVPHRQNNTSRKGMPOQKGSGWGRPHSNRFSRRDDSSSD 420
 Db 440 GPSHENITTHGRKYHYVPHRQNNTSRKGMPOQKGSGWGRPHSNRFSRRDDSSSD 499
 Qy 421 SGSSSESDGD 430
 Db 500 SGSSSESDGD 509

RESULT 3
 US-10-311-840-1
 ; Sequence 1, Application US/10311840
 ; Publication No. US20030175008A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KUROKAWA, Tomofumi
 ; APPLICANT: YAMADA, Takao
 ; APPLICANT: MORIZOTO, Shisetsu
 ; FILE OF INVENTION: No. US20030175808A1el Protein and its DNA
 ; TITLE OF INVENTION: US/2738010P
 ; CURRENT APPLICATION NUMBER: US/10/311, 840
 ; CURRENT FILING DATE: 2003-12-18
 ; PRIORITY NUMBER: PCT/JP01/05263
 ; PRIORITY PILING DATE: 2001-06-20
 ; PRIORITY APPLICATION NUMBER: JP 2000-191088
 ; SEQ ID NO 1
 ; NUMBER OF SEQ ID NOS: 10
 ; LENGTH: 525
 ; TYPE: PR
 ; ORGANISM: Human
 US-10-311-840-1

Query Match 99.9%; Score 2276; DB 12; Length 525;
 Best Local Similarity 99.8%; Pred. No. 4.5e-173;
 Matches 429; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNKYESISNKENTHGLRMSIYPKSTGNKGFDGDAISKLHDQEYGAIRNNQHIM 60
 Db 96 LNKEYSISNKENTHGLRMSIYPKSTGNKGFDGDAISKLHDQEYGAIRNNQHIM 155
 Qy 61 GPVTAIKLGEENKENTPRVNLTIPASNYAKASHDKKKPQDQSAQKSPVKSTHR 120
 Db 156 GPVTAIKLGEENKENTPRVNLTIPASNYAKASHDKKKPQDQSAQKSPVKSTHR 215
 Qy 121 IQRNIDYLKHLVKVKIPSDFEGSCYTDLQERGNDISPGDGOPFKD1PGKBEATGPD 180
 Db 216 IQRNIDYLKHLVKVKIPSDFEGSCYTDLQERGNDISPGDGOPFKD1PGKBEATGPD 275
 Qy 181 LEGDIQTGPAGPSAESTHLDTKKGYNEI PEREENGNTIGTDETAKEADAVDVLV 240
 Db 276 LEGDIQTGPAGPSAESTHLDTKKGYNEI PEREENGNTIGTDETAKEADAVDVLV 335
 Qy 241 EGSDNDIMGSTNFKELPGREGNRVDAAGSQAOKSPVKSTHR 300
 Db 336 EGSDNDIMGSTNFKELPGREGNRVDAAGSQAOKSPVKSTHR 395
 Qy 1 VNKYESISNKENTHGLRMSIYPKSTGNKGFDGDAISKLHDQEYGAIRNNQHIM 60
 Db 96 LNKEYSISNKENTHGLRMSIYPKSTGNKGFDGDAISKLHDQEYGAIRNNQHIM 155
 Qy 61 GPVTAIKLGEENKENTPRVNLTIPASNYAKASHDKKKPQDQSAQKSPVKSTHR 120
 Db 156 GPVTAIKLGEENKENTPRVNLTIPASNYAKASHDKKKPQDQSAQKSPVKSTHR 215
 Qy 121 IQRNIDYLKHLVKVKIPSDFEGSCYTDLQERGNDISPGDGOPFKD1PGKBEATGPD 180
 Db 216 IQRNIDYLKHLVKVKIPSDFEGSCYTDLQERGNDISPGDGOPFKD1PGKBEATGPD 275
 Qy 181 LEGDIQTGPAGPSAESTHLDTKKGYNEI PEREENGNTIGTDETAKEADAVDVLV 240
 Db 276 LEGDIQTGPAGPSAESTHLDTKKGYNEI PEREENGNTIGTDETAKEADAVDVLV 335
 Qy 301 YNEIPKNGKGSTRKGYDHNSRNQATLNKEQRFPSCKSKQSGLPIPSRGDNEIKNEMDSFN 360
 Db 396 YNEIPKNGKGSTRKGYDHNSRNQATLNKEQRFPSCKSKQSGLPIPSRGDNEIKNEMDSFN 455
 Qy 361 GPSHENITTHGRKYHYVPHRQNNTSRKGMPOQKGSGWGRPHSNRFSRRDDSSSD 420
 Db 456 GPSHENITTHGRKYHYVPHRQNNTSRKGMPOQKGSGWGRPHSNRFSRRDDSSSD 515
 Qy 421 SGSSSESDGD 430
 Db 516 SGSSSESDGD 525

RESULT 4
 US-09-794-422-46
 ; Sequence 46, Application US/097944422
 ; Publication No. US20030166239A1.
 ; GENERAL INFORMATION:
 ; APPLICANT: Brown, Thomas A.
 ; APPLICANT: De Wet, Jeffrey R.
 ; APPLICANT: Gowen, Lori C.
 ; APPLICANT: Hames, Lynn M.
 ; TITLE OF INVENTION: Mammalian Osteoregulins
 ; FILE REFERENCE: PC10445
 ; CURRENT APPLICATION NUMBER: US/09/794,422
 ; CURRENT FILING DATE: 2001-02-27
 ; PRIORITY APPLICATION NUMBER: 60/185,617
 ; PRIORITY FILING DATE: 2000-09-22
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 46
 ; LENGTH: 540
 ; TYPE: PPT
 ; ORGANISM: Homo sapiens
 US-09-794-422-46

Query Match 99.9%; Score 2276; DB 12; Length 556;
 Best Local Similarity 99.8%; Pred. No. 4.7e-173;
 Matches 429; Conservative 1; Mis matches 0; Indels 0; Gaps 0;

Qy 1 VNKYESISNKENTHGLRMSIYPKSTGNKGFDGDDAIASKLHDQEYGA
 Db 127 LNKEYSISNKENTHGLRMSIYPKSTGNKGFDGDDAIASKLHDQEYGA
 Db 61 GPVTAIKLGEENKENTPRVNLTIPASMYAKAHSDKKPORDSQAKSPY
 Qy 1 VNKYESISNKENTHGLRMSIYPKSTGNKGFDGDDAIASKLHDQEYGA
 Db 187 GPVTAIKLGEENKENTPRVNLTIPASMYAKAHSDKKPORDSQAKSPY
 Db 121 JOHNIDYLKHLSKVKKIPSDFEGSGTYDQERGDNDISPFSGDQC
 Qy 247 QHNDIYKHLSKVKKISDFEGSGTYDQERGDNDISPFSGDQC
 Db 111 LNKEYSISNKENTHGLRMSIYPKSTGNKGFDGDDAIASKLHDQEY
 Db 307 LEGKDIDQTFAGPSEAESTHLDTKPGTGYNEIPREENGNTIGR
 Qy 181 LEGKDIDQTFAGPSEAESTHLDTKPGTGYNEIPREENGNTIGR
 Db 171 GPVTAIKLGEENKENTPRVNLTIPASMYAKHSKDKKKPORDSO
 Db 367 EGSDNDIMSTNFNKELPGEGRNTRDGSNAHQCKV
 Qy 121 JOHNIDYLKHLSKVKKIPSDFEGSGTYDQERGDNDISPFSGDQC
 Db 171 GPVTAIKLGEENKENTPRVNLTIPASMYAKHSKDKKKPORDSO
 Db 231 QHNDIYKHLSKVKKIPSDFEGSGTYDQERGDNDISPFSGDQC
 Db 291 LEGKDIDQTFAGPSEAESTHLDTKPGTGYNEIPREENGNTIGR
 Db 351 EGSDNDIMSTNFNKELPGEGRNTRDGSNAHQCKV
 Qy 241 YNEIPKNGKGSTRKGVDHSNRNQATLNKEQRFPSSKGQS
 Db 427 YNEIPKNGKGSTRKGVDHSNRNQATLNKEQRFPSSKGQS
 Qy 291 LEGKDIDQTFAGPSEAESTHLDTKPGTGYNEIPREENGNTIGR
 Db 351 EGSDNDIMSTNFNKELPGEGRNTRDGSNAHQCKV
 Qy 301 YNEIPKNGKGSTRKGVDHSNRNQATLNKEQRFPSSKGQS
 Db 421 SGSSSESQGD 430
 Qy 361 GPSHENILTHGRKYHYPHRONNSTRKGMPQCKGSW
 Db 487 GPSHENILTHGRKYHYPHRONNSTRKGMPQCKGSW
 Qy 351 EGSDNDIMSTNFNKELPGEGRNTRDGSNAHQCKV
 Db 547 SGSSSESQGD 556

RESULT 5
 US-09-794-422-46
 ; Sequence 8, Application US/09794422
 ; Publication No. US20030166239A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brown, Thomas A.
 ; APPLICANT: De Wet, Jeffrey R.
 ; APPLICANT: Gowen, Lori C.
 ; APPLICANT: Hames, Lynn M.
 ; TITLE OF INVENTION: Mammalian Osteoregulins
 ; FILE REFERENCE: PC10445

Query Match 99.9%; Score 2276; DB 12; Length 556;
 Best Local Similarity 99.8%; Pred. No. 4.7e-173;
 Matches 429; Conservative 1; Mis matches 0; Indels 0; Gaps 0;

Qy 1 VNKYESISNKENTHGLRMSIYPKSTGNKGFDGDDAIASKLHDQEYGA
 Db 127 LNKEYSISNKENTHGLRMSIYPKSTGNKGFDGDDAIASKLHDQEYGA
 Db 61 GPVTAIKLGEENKENTPRVNLTIPASMYAKAHSDKKPORDSQAKSPY
 Qy 1 VNKYESISNKENTHGLRMSIYPKSTGNKGFDGDDAIASKLHDQEYGA
 Db 187 GPVTAIKLGEENKENTPRVNLTIPASMYAKAHSDKKPORDSQAKSPY
 Db 121 JOHNIDYLKHLSKVKKIPSDFEGSGTYDQERGDNDISPFSGDQC
 Qy 247 QHNDIYKHLSKVKKISDFEGSGTYDQERGDNDISPFSGDQC
 Db 111 LNKEYSISNKENTHGLRMSIYPKSTGNKGFDGDDAIASKLHDQEY
 Db 307 LEGKDIDQTFAGPSEAESTHLDTKPGTGYNEIPREENGNTIGR
 Qy 181 LEGKDIDQTFAGPSEAESTHLDTKPGTGYNEIPREENGNTIGR
 Db 171 GPVTAIKLGEENKENTPRVNLTIPASMYAKHSKDKKKPORDSO
 Db 367 EGSDNDIMSTNFNKELPGEGRNTRDGSNAHQCKV
 Qy 121 JOHNIDYLKHLSKVKKIPSDFEGSGTYDQERGDNDISPFSGDQC
 Db 171 GPVTAIKLGEENKENTPRVNLTIPASMYAKHSKDKKKPORDSO
 Db 231 QHNDIYKHLSKVKKIPSDFEGSGTYDQERGDNDISPFSGDQC
 Db 291 LEGKDIDQTFAGPSEAESTHLDTKPGTGYNEIPREENGNTIGR
 Db 351 EGSDNDIMSTNFNKELPGEGRNTRDGSNAHQCKV
 Qy 241 YNEIPKNGKGSTRKGVDHSNRNQATLNKEQRFPSSKGQS
 Db 427 YNEIPKNGKGSTRKGVDHSNRNQATLNKEQRFPSSKGQS
 Qy 291 LEGKDIDQTFAGPSEAESTHLDTKPGTGYNEIPREENGNTIGR
 Db 351 EGSDNDIMSTNFNKELPGEGRNTRDGSNAHQCKV
 Qy 301 YNEIPKNGKGSTRKGVDHSNRNQATLNKEQRFPSSKGQS
 Db 421 SGSSSESQGD 430
 Qy 361 GPSHENILTHGRKYHYPHRONNSTRKGMPQCKGSW
 Db 487 GPSHENILTHGRKYHYPHRONNSTRKGMPQCKGSW
 Qy 351 EGSDNDIMSTNFNKELPGEGRNTRDGSNAHQCKV
 Db 547 SGSSSESQGD 556

RESULT 6
 US-09-794-422-46
 ; Sequence 2, Application US/09814550
 ; Publication No. US20020102641A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schiavi, Susan
 ; APPLICANT: Madden, Stephen
 ; APPLICANT: Manavalan, Parthasarathy
 ; APPLICANT: Levine, Michael
 ; APPLICANT: Jan de Beur, Suzanne
 ; TITLE OF INVENTION: ONCOGENIC OSTEOMALACIA-RELATED GENE 1
 ; FILE REFERENCE: 5014US

Query Match 99.9%; Score 2276; DB 12; Length 556;
 Best Local Similarity 99.8%; Pred. No. 4.7e-173;
 Matches 429; Conservative 1; Mis matches 0; Indels 0; Gaps 0;

Qy 1 VNKYESISNKENTHGLRMSIYPKSTGNKGFDGDDAIASKLHDQEYGA
 Db 127 LNKEYSISNKENTHGLRMSIYPKSTGNKGFDGDDAIASKLHDQEYGA
 Db 61 GPVTAIKLGEENKENTPRVNLTIPASMYAKAHSDKKPORDSQAKSPY
 Qy 1 VNKYESISNKENTHGLRMSIYPKSTGNKGFDGDDAIASKLHDQEYGA
 Db 187 GPVTAIKLGEENKENTPRVNLTIPASMYAKAHSDKKPORDSQAKSPY
 Db 121 JOHNIDYLKHLSKVKKIPSDFEGSGTYDQERGDNDISPFSGDQC
 Qy 247 QHNDIYKHLSKVKKISDFEGSGTYDQERGDNDISPFSGDQC
 Db 111 LNKEYSISNKENTHGLRMSIYPKSTGNKGFDGDDAIASKLHDQEY
 Db 307 LEGKDIDQTFAGPSEAESTHLDTKPGTGYNEIPREENGNTIGR
 Qy 181 LEGKDIDQTFAGPSEAESTHLDTKPGTGYNEIPREENGNTIGR
 Db 171 GPVTAIKLGEENKENTPRVNLTIPASMYAKHSKDKKKPORDSO
 Db 367 EGSDNDIMSTNFNKELPGEGRNTRDGSNAHQCKV
 Qy 121 JOHNIDYLKHLSKVKKIPSDFEGSGTYDQERGDNDISPFSGDQC
 Db 171 GPVTAIKLGEENKENTPRVNLTIPASMYAKHSKDKKKPORDSO
 Db 231 QHNDIYKHLSKVKKIPSDFEGSGTYDQERGDNDISPFSGDQC
 Db 291 LEGKDIDQTFAGPSEAESTHLDTKPGTGYNEIPREENGNTIGR
 Db 351 EGSDNDIMSTNFNKELPGEGRNTRDGSNAHQCKV
 Qy 241 YNEIPKNGKGSTRKGVDHSNRNQATLNKEQRFPSSKGQS
 Db 427 YNEIPKNGKGSTRKGVDHSNRNQATLNKEQRFPSSKGQS
 Qy 291 LEGKDIDQTFAGPSEAESTHLDTKPGTGYNEIPREENGNTIGR
 Db 351 EGSDNDIMSTNFNKELPGEGRNTRDGSNAHQCKV
 Qy 301 YNEIPKNGKGSTRKGVDHSNRNQATLNKEQRFPSSKGQS
 Db 421 SGSSSESQGD 430
 Qy 361 GPSHENILTHGRKYHYPHRONNSTRKGMPQCKGSW
 Db 487 GPSHENILTHGRKYHYPHRONNSTRKGMPQCKGSW
 Qy 351 EGSDNDIMSTNFNKELPGEGRNTRDGSNAHQCKV
 Db 547 SGSSSESQGD 556

RESULT 7
 US-09-794-422-46
 ; Sequence 8, Application US/09794422
 ; Publication No. US20030166239A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brown, Thomas A.
 ; APPLICANT: De Wet, Jeffrey R.
 ; APPLICANT: Gowen, Lori C.
 ; APPLICANT: Hames, Lynn M.
 ; TITLE OF INVENTION: Mammalian Osteoregulins
 ; FILE REFERENCE: PC10445

; TYPE: PRT ; ORGANISM: Homo sapiens US-09-14-550-2

Query Match 99.6%; Score 2269; DB 10; Length 525;
Best Local Similarity 99.5%; Pred. No. 1.6e-172;
Matches 428; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VNKYESISKENTINGLMSIYPKSTGNKGFDGDDASKLHQBEYGAALLRNMQHIM 60
Db 96 LNKEYSISKENTINGLMSIYPKSTGNKGFDGDDASKLHQBEYGAALLRNMQHIM 155

Qy 61 GPVTAIKLIGEENKENTPNVLNITPASMYAHSKDKKKPORDSQAQSPVYKS 120
Db 156 GPVTAIKLIGEENKENTPNVLNITPASMYAHSKDKKKPORDSQAQSPVYKS 215

Qy 121 IQRNIDYLGHLSKVTKIPDFEGSGYTDLQERGNDISPSFGDQPFKDIPGKGEATGPD 180
Db 216 IQRNIDYLGHLSKVTKIPDFEGSGYTDLQERGNDISPSFGDQPFKDIPGKGEATGPD 275

Qy 181 LEGKDIQTFAGPSEAESTHLDTKPGYNEIPEREEGNTIGTRDEAKEADAVSYL 240
Db 276 LEGKDIQTFAGPSEAESTHLDTKPGYNEIPEREEGNTIGTRDEAKEADAVSYL 335

Qy 241 EGNDIMGSTNFNKELPGRIGNRVDAGSONAHOGKVEFHYPAPSKEKEGGSSDAESTN 300
Db 336 EGNDIMGSTNFNKELPGRIGNRVDAGSONAHOGKVEFHYPAPSKEKEGGSSDAESTN 395

Qy 301 YNEIPKNGKGSTRKGVDHESNRNQATLNKEORFSPKGSKSCLPISGLPNSRGLDNEINEMDSFN 360
Db 396 YNEIPKNGKGSTRKGVDHESNRNQATLNKEORFSPKGSKSCLPISGLPNSRGLDNEINEMDSFN 455

Qy 361 GPSHENITHGRKYHYVPHRNNSTRNKGMPQKGWSGRQPHSNRRDDSSSD 420
Db 456 GPSHENITHGRGYHYVPHRNNSTRNKGMPQKGWSGRQPHSNRRDDSSSD 515

Qy 421 SGSSSESDGD 430
Db 516 SGSSSESDGD 525

RESULT 7 US-09-794-422-4

; Sequence 4, Application US/09/794,422
; CURRENT APPLICATION NUMBER: US/09/794,422
; PRIORITY INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hanes, Lynn M.
; FILE REFERENCE: PC10445
; TITLE OF INVENTION: Mammalian Osteoregulins
; CURRENT APPLICATION NUMBER: US/09/794,422
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-794-422-4

Query Match 43.2%; Score 983.5; DB 12; Length 441;
Best Local Similarity 50.5%; Pred. No. 3.6e-70;
Matches 217; Conservative 52; Mismatches 134; Indels 27; Gaps 8;

Qy 6 SISNKENTINGLMSIYPKSTGNKGFDGDDASKLHQBEYGAALLRNMQHIMGPUTA 65
Db 34 SCGRQDSTKDLAASVYPPPTVDEGTGCGDQGDRYGAALLRNQTVFKSLVYTG 93

Qy 66 IKLIGEENKENTPNVLNITPASMYAHSKDKKKPORDSQAQSPVYKS--KSTHRIQ 122
Db 94 AELRREGNQEKRPOSVLSPVADVNDAKVSLSKQIKNQESYLLTQSSPVYKSHTKHTRQTR 153

Qy 123 HNDYDYLGHLSKVTKIPDSDFEGSGYTDLQERGNDISPSFGDQPFKDIPGKGEA-TGPDPL 181
Db 154 RSTHYLTHLPQIKKTPSDLEGSSPDLLVRGNDVPPFGDQGHMFHPIPGKGGAGSGP- 212

Qy 182 EGKDIQTFAGPSEAESTHLDTKPGYNEIPEREEGNTIGTRDEAKEADAVSYLVE 241
Db 213 --SSTRPLGSSSAEVDPHMSGLGSNEIPGRBGGSSAYATRDKAAGAGSAGSLVG 270

Qy 242 GSNDIMGSTNFNKELPGRGENRYDAGSONAHOGKVEFHYPAPSKEKEGGSSDAESTN 301
Db 271 GSNEITGTSNFRELPKGECNRINAGSQNAHOGKVEFHYPQVAEREVKRGGEVHAGRA-GY 329

Qy 302 NEIPKNGKGSTRKGVDHESNRNQATLNKEORFSPKGSKSCLPISGLPNSRGLDNEINEMDSFPN 361
Db 330 NEIPKSSKGSSSDAAEESKGNLTLTASQRFPKGSKSCLPALSNSNEVKSE- 383

Qy 362 PSHENITHGRKYHYVPHRNNSTRNKGMPQKGWSGRQPHSNRRDDSSSD 420
Db 384 --EN--HYVFHGQNNLTNPNGMSQRGGSWPSRRPNSHRASTRQR-DSESSS 431

Qy 421 SGSSSESDGD 430
Db 432 SGSSSESDGD 441

RESULT 8 US-09-794-422-2

; Sequence 2, Application US/09/794,422
; Sequence 2, Application US/09/794,422
; Publication No. US20030166239A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hanes, Lynn M.
; FILE REFERENCE: PC10445
; CURRENT APPLICATION NUMBER: US/09/794,422
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-794-422-2

Query Match 41.2%; Score 938.5; DB 12; Length 435;
Best Local Similarity 49.4%; Mismatches 45; Indels 14; Gaps 8;

Qy 9 NKENTHNGLMSIYPKSTGNKGFDGDDASKLHQBEYGAALRNMQHIMGPUTA 68
Db 29 NQENTH--LASTKPEPMVKGCTEGRGRDAPLFLDQNRRQATILRLNTQPVKSLVGTREV 85

Qy 69 LGRENKENTPNVLNITPASMYAHSKDKKKPORDSQAQSPVYKSHTKHTRQTR 128
Db 86 QSDRNKEKIPDSDFEGSGYTDLQERGNDISPSFGDQPFKDIPGKGEATGPDE--GKD 145

Qy 129 KHLISKVTKIPDSDFEGSGYTDLQERGNDISPSFGDQPFKDIPGKGEATGPDE--GKD 185
Db 146 THPQIKLSDPFSASPDLLVRGNDVPPFGDQGHMFHPIPGKGGAGSGP-DESSA 205

Qy 186 IQTGEAGPSEAESTHLDTKPGYNEIPEREEGNTIGTRDEAKEADAVSYLVEGSND 245

Software: FastSEQ for Windows Version 4.0

SEQ ID NO 2 ; Software: FastSEQ for Windows Version 4.0
 LENGTH: 47 ;
 TYPE: PRT ;
 ORGANISM: Artificial Sequence ;
 FEATURE: Peptidic compound ;
 OTHER INFORMATION: Peptidic compound
 US-09-812-485A-2

Query Match 10.8%; Score 246; DB 10; Length 47;
 Best Local Similarity 100.0%; Pred. No. 1..1e-12;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 AQKSPVSKSKSTRIQNIDYLKHLSTVKKIPSDFEFGSGYTDLQERGD 154
 Db 1 AQKSPVSKSKSTRIQNIDYLKHLSTVKKIPSDFEFGSGYTDLQERGD 47

RESULT 11

US-09-812-485A-4 ; Sequence 4, Application US/09812485A
 ; Publication No. US20020197267A1
 GENERAL INFORMATION:
 ; APPLICANT: Kumagai, Yoshinari ;
 ; Blacher, Russell ;
 ; Yoneda, Toshiyuki ;
 TITLE OF INVENTION: Integrin Binding Motif Containing Peptides and Methods of Treating Skeletal Diseases
 ; TITLE OF INVENTION: Peptides and Methods of Treating Skeletal Diseases
 ; FILE REFERENCE: BEAR-006CIP
 ; CURRENT APPLICATION NUMBER: US/09/812,485A
 ; CURRENT FILING DATE: 2001-03-19
 ; PRIOR APPLICATION NUMBER: 09/641,034
 ; PRIOR FILING DATE: 2000-08-16
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 47
 ; TYPE: PRT ;
 ; ORGANISM: Artificial Sequence ;
 ; FEATURE: Peptidic compound ;
 ; OTHER INFORMATION: peptidic compound
 US-09-812-485A-4

Query Match 10.3%; Score 235.5; DB 10; Length 47;
 Best Local Similarity 94.0%; Pred. No. 7.3e-12;
 Matches 47; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 105 DSQACKSPVSKSKSTRIQNIDYLKHLSTVKKIPSDFEFGSGYTDLQERGD 154
 Db 1 DSQACKSPVSKSKSTRIQNIDYLKHLSTVKKIPSDFEFGSGYTDLQERGD 47

RESULT 12

US-09-812-485A-3 ; Sequence 3, Application US/09812485A
 ; Publication No. US20020197267A1
 GENERAL INFORMATION:
 ; APPLICANT: Kumagai, Yoshinari ;
 ; Blacher, Russell ;
 ; Yoneda, Toshiyuki ;
 TITLE OF INVENTION: Integrin Binding Motif Containing Peptides and Methods of Treating Skeletal Diseases
 ; TITLE OF INVENTION: Peptides and Methods of Treating Skeletal Diseases
 ; FILE REFERENCE: BEAR-006CIP
 ; CURRENT APPLICATION NUMBER: US/09/812,485A
 ; CURRENT FILING DATE: 2001-03-19
 ; PRIOR APPLICATION NUMBER: 09/641,034
 ; PRIOR FILING DATE: 2000-08-16
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 47
 ; TYPE: PPT ;
 ; ORGANISM: Artificial Sequence

RESULT 13

US-09-812-485A-2 ; Sequence 2, Application US/09812485A
 ; Publication No. US20020197267A1
 GENERAL INFORMATION:
 ; APPLICANT: Kumagai, Yoshinari ;
 ; Blacher, Russell ;
 ; Yoneda, Toshiyuki ;
 TITLE OF INVENTION: Integrin Binding Motif Containing Peptides and Methods of Treating Skeletal Diseases
 ; TITLE OF INVENTION: Peptides and Methods of Treating Skeletal Diseases
 ; FILE REFERENCE: BEAR-006CIP
 ; CURRENT APPLICATION NUMBER: US/09/812,485A
 ; CURRENT FILING DATE: 2001-03-19
 ; PRIOR APPLICATION NUMBER: 09/641,034
 ; PRIOR FILING DATE: 2000-08-16
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 47
 ; TYPE: PPT ;
 ; ORGANISM: Artificial Sequence

Db 206 V---SGSSNVIEVDPTINGLGSNEIPGRGHIGGATRGIKTAQQGAGSADVSLVEGSNE 261

QY 246 IMGSTNPKEPLLPGREGNRVDAQSONAHQCKVPEHYPPAPSKEKRKEGSSDAESTVNINP 305
 Db 262 1TGSTKFRELPKEGRGVDAQSONAHQCKVPEHYQAPSKEKVKGGSREHTGRAGYNEP 321

QY 306 KNGKGSRKDGVHDHSRNQATNEKQRPFPSKGSKQGLP1PSRGDNETKNEMDSFNGPHE 365
 Db 322 ESSKGAGSKDAEESKGQVTLTESQRFKGKGSQ---SHSLGNEVKSSEDDSSNLARE 377

QY 366 NI-IITHGRKYHYPHRQNNSTRKNGMPOKGWSN-GROPHSNRPFSSRRDSDSSSDGS 423
 Db 378 GAIAHRRRTSH-----PTRNRMQSRRGMSASRRBPHRRVSTR-DSSESSSSGS 428

QY 424 SSESDDG 430
 Db 429 SSESDDG 435

QY 429 SSESDDG 435

RESULT 9

US-09-812-485A-1 ; Sequence 1, Application US/09812485A
 ; Publication No. US20020197267A1
 GENERAL INFORMATION:
 ; APPLICANT: Kumagai, Yoshinari ;
 ; Blacher, Russell ;
 ; Yoneda, Toshiyuki ;
 TITLE OF INVENTION: Integrin Binding Motif Containing Peptides and Methods of Treating Skeletal Diseases
 ; TITLE OF INVENTION: Peptides and Methods of Treating Skeletal Diseases
 ; FILE REFERENCE: BEAR-006CIP
 ; CURRENT APPLICATION NUMBER: US/09/812,485A
 ; CURRENT FILING DATE: 2001-03-19
 ; PRIOR APPLICATION NUMBER: 09/641,034
 ; PRIOR FILING DATE: 2000-08-16
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 97
 ; TYPE: PRT ;
 ; ORGANISM: Artificial Sequence ;
 ; FEATURE:
 ; OTHER INFORMATION: Peptidic compound
 US-09-812-485A-1

Query Match 22.6%; Score 514; DB 10; Length 97;
 Best Local Similarity 100.0%; Pred. No. 1.2e-33;
 Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 DSQACKSPVSKSKSTRIQNIDYLKHLSTVKKIPSDFEFGSGYTDLQERGD 164
 Db 1 DSQACKSPVSKSKSTRIQNIDYLKHLSTVKKIPSDFEFGSGYTDLQERGD 60

QY 165 QPKFDIPGKCEATGPDELEGKD1QTGFAGPSRAESTHL 201
 Db 61 QPKFDIPGKCEATGPDELEGKD1QTGFAGPSRAESTHL 97

RESULT 10

US-09-812-485A-2 ; Sequence 2, Application US/09812485A
 ; Publication No. US20020197267A1
 GENERAL INFORMATION:
 ; APPLICANT: Kumagai, Yoshinari ;
 ; Blacher, Russell ;
 ; Yoneda, Toshiyuki ;
 TITLE OF INVENTION: Integrin Binding Motif Containing Peptides and Methods of Treating Skeletal Diseases
 ; TITLE OF INVENTION: Peptides and Methods of Treating Skeletal Diseases
 ; FILE REFERENCE: BEAR-006CIP
 ; CURRENT APPLICATION NUMBER: US/09/812,485A
 ; CURRENT FILING DATE: 2001-03-19
 ; PRIOR APPLICATION NUMBER: 09/641,034
 ; PRIOR FILING DATE: 2000-08-16
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 47
 ; TYPE: PPT ;
 ; ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: peptidic compound
US-09-812-485A-3

Query Match Similarity 10.0%; Score 229; DB 10; Length 47;
Best Local Similarity 100.0%; Pred. No. 2.4e-11;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 108 AQKSPVKSSTRIQHNIDYLKHLISKYKKIKPSDFEGSGYTDLQE 151
Db 4 AKSPVKSSTRIQHNIDYLKHLISKYKKIKPSDFEGSGYTDLQE 47

RESULT 13
US-09-812-485A-23
Sequence 23, Application US/09812485A
Publication No. US20020197267A1
GENERAL INFORMATION:
APPLICANT: Kumagai, Yoshinari
APPLICANT: Blacher, Russell
APPLICANT: Yoneda, Toshiyuki
TITLE OF INVENTION: Integrin Binding Motif Containing Skeletal Diseases
FILE REFERENCE: BEAR-006CIP
CURRENT APPLICATION NUMBER: US/09/812,485A
PRIORITY FILING DATE: 2001-03-19
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 23
LENGTH: 0
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: peptidic compound
US-09-812-485A-23

Query Match Similarity 100.0%; Score 229; DB 10; Length 47;
Best Local Similarity 100.0%; Pred. No. 2.4e-11;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 DSQAQSPVKSKSTRIQHNIDYLKHLISKYKKIKPSDFEGSGYTDLQE 154
Db 1 DSQAQSPVKSKSTRIQHNIDYLKHLISKYKKIKPSDFEGSG-----RGD 44

RESULT 15
US-09-812-485A-5
Sequence 5, Application US/09812485A
Publication No. US20020197267A1
GENERAL INFORMATION:
APPLICANT: Kumagai, Yoshinari
APPLICANT: Blacher, Russell
APPLICANT: Yoneda, Toshiyuki
TITLE OF INVENTION: Integrin Binding Motif Containing Skeletal Diseases
FILE REFERENCE: BEAR-006CIP
CURRENT APPLICATION NUMBER: US/09/812,485A
PRIORITY FILING DATE: 2001-03-19
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 5
LENGTH: 44
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: peptidic compound
US-09-812-485A-5

Query Match Similarity 100.0%; Score 215; DB 10; Length 44;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 111 SPVKSKSTRIQHNIDYLKHLISKYKKIKPSDFEGSGYTDLQE 151
Db 4 SPVKSKSTRIQHNIDYLKHLISKYKKIKPSDFEGSGYTDLQE 44

Search completed: November 26, 2003, 15:53:39
Job time : 38 secs

RESULT 14
US-09-812-485A-6
Sequence 6, Application US/09812485A
Publication No. US20020197267A1
GENERAL INFORMATION:
APPLICANT: Kumagai, Yoshinari
APPLICANT: Blacher, Russell
APPLICANT: Yoneda, Toshiyuki
TITLE OF INVENTION: Integrin Binding Motif Containing Skeletal Diseases
FILE REFERENCE: BEAR-006CIP
CURRENT APPLICATION NUMBER: US/09/812,485A
PRIORITY FILING DATE: 2001-03-19
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 6
LENGTH: 44
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: peptidic compound
US-09-812-485A-6

Query Match Similarity 9.6%; Score 218; DB 10; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 152 RGDNNDISPPSGDQPFKDXDIPGKGEATGPDLLEGKDIQTGFA 191
Db 1 RGDNNDISPPSGDQPFKDXDIPGKGEATGPDLLEGKDIQTGFA 40

RESULT 14
US-09-812-485A-6
Sequence 6, Application US/09812485A
Publication No. US20020197267A1
GENERAL INFORMATION:
APPLICANT: Kumagai, Yoshinari
APPLICANT: Blacher, Russell
APPLICANT: Yoneda, Toshiyuki
TITLE OF INVENTION: Integrin Binding Motif Containing Skeletal Diseases
FILE REFERENCE: BEAR-006CIP
CURRENT APPLICATION NUMBER: US/09/812,485A
PRIORITY FILING DATE: 2001-03-19
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 6
LENGTH: 44
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: peptidic compound
US-09-812-485A-6

Query Match Similarity 9.5%; Score 216; DB 10; Length 44;

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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 29, 2003, 22:43:06 ; Search time 83 Seconds

(without alignments)

2286 684 Million cell updates/sec

Title: US-09-700-696C-2

Perfect score: 2279

Sequence: 1 VNKYESISNKENTHNLRMS.....RRDSSSESDGSSSESDGD 430

Scoring table: BLASTNM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delet 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL:frame+ p2n.model -DEV=xlh

-Q= /cgn2_1/USPTO_spool/US09700696/runat_26112003_152633_14643/app/query.fasta_1.583

-DB=Issued_Patents_NA -QPMFT=fastap -SUFIX=_0.1 -LOOFCL=0

-LQOPENT=0 -UNITS=Bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi

-LIST=45 -DOCALIGN=200 -THR SCORE=PCT -PCT -THR MAX=100 -THR MIN=0 ALIGNN=15

-MDB=LOCAL -OUTFN=ptc -NORM=ext -HEAPSIZE=500 -MAXLEN=3000000000

-USER=US09700696 @CGN 1 1.56 @runat_26112003_152633_14643 -NCPU=6 -ICPU=3

-NO MMAP -LARGEQUERY -NEG -SCORES=0 -WAIT -DSFBLOCK=100 -LONGLOG

-DEV TIMEOUT=30 -WARN=30 -TREADS=1 -XGAPEXT=0.5 -FGAPOP=6

-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -FGAPOP=6 -DELOP=6 -DELETE=7

Database : Issued_Patents_NA:*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	Match ID	Description
1	150	6.6	6755 3 US-08-931-999-4	Sequence 4, Appli
2	140	6.1	2650 1 US-08-524-757-11	Sequence 11, Appli
3	138.5	6.1	2384 1 US-07-814-964-10	Sequence 10, Appli
4	138.5	6.1	2384 1 US-08-258-442-10	Sequence 10, Appli
5	138.5	6.1	2384 1 US-08-328-809-5	Sequence 5, Appli
6	138.5	6.1	2384 4 US-08-866-840-5	Sequence 10, Appli
7	138.5	6.1	2384 5 PCT-US92-11107-10	Sequence 10, Appli
8	137	6.0	9370 1 US-08-320-559-27	Sequence 27, Appli
9	137	6.0	9370 3 US-08-545-860D-27	Sequence 27, Appli
10	137	6.0	9370 5 PCT-US94-04496-27	Sequence 27, Appli
11	137	6.0	9391 1 US-08-320-559-25	Sequence 25, Appli
12	137	6.0	9391 3 US-08-545-860D-25	Sequence 25, Appli

INFORMATION FOR SEQ ID NO: 4:

13 137 6.0 9391 5 PCT-US94-04496-25 Sequence 25, Appli
 14 134.5 5.9 4084 2 US-08-568-459A-1 Sequence 1, Appli
 15 134.5 5.9 4084 2 US-09-210-826B-1 Sequence 1, Appli
 16 134.5 5.9 4084 6 5198347-5 Patent No. 5198347
 17 134.5 5.9 4084 6 5198347-3 Patent No. 5198347
 18 129 5.7 3157 6 5198347-3 Sequence 1, Appli
 19 127.5 5.6 3707 4 US-08-118-101A-1 Sequence 3, Appli
 20 127 5.6 2695 4 US-09-706-197-3 Sequence 295, App
 21 127 5.6 4215 4 US-09-620-312D-295 Sequence 12, Appli
 22 126.5 5.6 1393 5 PCT-US93-01261-12 Sequence 1, Appli
 23 126.5 5.6 3773 3 US-09-130-242-1 Sequence 3, Appli
 24 125.5 5.5 3825 3 US-09-208-742-3 Sequence 2, Appli
 25 125.5 5.5 5173 4 US-08-301-08-2 Sequence 693, App
 26 124.5 5.5 3552 4 US-09-134-001C-693 Sequence 11, Appli
 27 123 5.4 1503 3 US-08-999-774A-11 Sequence 1269, Ap
 28 123 5.4 3534 4 US-08-134-001C-2269 Sequence 10, Appli
 29 123 5.4 4766 5 PCT-US93-07261-10 Sequence 18, Appli
 30 123 5.4 6775 4 US-09-620-312D-289 Sequence 289, App
 31 122.5 5.4 3347 4 US-09-736-457-318 Sequence 318, App
 32 122.5 5.4 2073 4 US-09-134-001C-1731 Sequence 1731, Ap
 33 122 5.4 43280 2 US-08-804-227C-1 Sequence 18, Appli
 34 122 5.4 2004 1 US-08-471-033-18 Sequence 18, Appli
 35 121 5.3 2004 2 US-08-471-044-18 Sequence 18, Appli
 36 121 5.3 2004 2 US-08-471-046A-18 Sequence 18, Appli
 37 121 5.3 2004 2 US-08-471-0483A-18 Sequence 18, Appli
 38 121 5.3 2004 2 US-08-470-566B-18 Sequence 18, Appli
 39 121 5.3 2004 2 US-08-469-334-18 Sequence 18, Appli
 40 121 5.3 2004 3 US-09-300-529-18 Sequence 18, Appli
 41 121 5.3 2655 1 US-08-471-033-17 Sequence 17, Appli
 42 121 5.3 2655 2 US-08-471-044-17 Sequence 17, Appli
 43 121 5.3 2655 2 US-08-463-483A-17 Sequence 17, Appli
 44 121 5.3 2655 2 US-08-471-046A-17 Sequence 17, Appli
 45 121 5.3 2655 2 US-08-471-046A-17 Sequence 17, Appli

ALIGNMENTS

RESULT 1
 US-08-911-999-4
 ; Sequence 4, Application US/08931999
 ; Patent No. 604219
 ; GENERAL INFORMATION:
 ; APPLICANT: Landolo, John J.
 ; TITLE OF INVENTION: Broad Spectrum Chemotherapeutic Peptide
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS: 4
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; ZIP: 64108
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hovey, Williams, Timmons & Collins
 ; STREET: 2405 Grand Boulevard, Suite 400
 ; CITY: Kansas City
 ; STATE: Missouri
 ; COUNTRY: U.S.A.
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/931,999
 ; FILING DATE: 19-SEP-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Collins, John M.
 ; REGISTRATION NUMBER: 26,262
 ; REFERENCE DOCUMENT NUMBER: 25043-A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 816/474-9050
 ; TELEFAX: 816/474-9057
 ; INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
 LENGTH: 6755 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: unknown
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: *Staphylococcus aureus*
 STRAIN: UT0007
 US-08-931-999-4

Alignment Scores:
 Pred. No.: 0.000155 Length: 6755
 Score: 150.00 Matches: 104
 Percent Similarity: 31.05% Conservative: 59
 Best Local Similarity: 19.81% Mismatches: 201
 Query Match: 6.58% Indels: 162
 DB: 3 Gaps: 20

US-09-700-696C-2 (1-430) x US-08-931-999-4 (1-6755)

Qy 2 AsnLysglutYrSerIleSerAsnLysGluAsnThrHisAsnGlyLeuArgMetSerIle 21
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 4164 AACCAAAACACAGAACGGAAAGCAACCCACAAACGACAAGGCCAA----- 4217

Qy 22 TyrProlysserThrGlyAsnLysGlyaspGlyaspGlyaspGlyaspLysLeu 41
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 4218 -----AAGGAAAACGGGGCAA-----AACGACCACAAAAAACAAACAA 4259

Qy 42 HisAspGlnGlu----- 45
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 Db 4260 CAAAGAGGAAAGCCACGCCAACGACAAACAGCCGAGCAAAACCCAGAAACAAA 4319

Qy 46 --GlutYrGlyAlaAlaLeuIleArgAsnAsnMetGlnHistileMetGlyProValThr 64
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 4320 GAAAAGCCGAAAAAAAGCACAAAGCCAAAGAACAGGAAAGCGGGAAAAA 4379

Qy 65 AlalleLysLeuIleGlyGluAsnLysGluAsnThrProArgAsnValLeuAsnIle 84
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 4380 AGAGAAA-----AAAAGCAAAACAGGAGAACCCCAACAAACAGCAAAACAA 4433

Qy 85 TieProAlaserMetAsnTyrAlaLysHisSerLysAspLysLysProGlnArg 104
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 4434 CAAGGAGCACAGGAAAAGGGAAACCCAGAGAAAACAAACAAACAAACAA 4493

Qy 105 AspSerGlnAlaGln-----Lys 110
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 4494 GAAGGAAACCAACGAGGAGGGCAACACACAAAGGCGGAGACGGAGAAA 4553

Qy 111 SerProVallys-----SerLysSerThrHisArgIleGlnHisAsn 124
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 4554 ACACCCGGAAAAAACACAAACACAAAGACACACAAACACAAAGAAC 4613

Qy 125 TieAspTyrIleIlySlysLeuSerLysLysProSerAppPheGluGlySer 144
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 4614 -----ACACGAAAAA-----GAAAACGGGGAGGGAGA 4643

Qy 145 GlyTyrThrAspIleGlnGluArgGlyAspAspIleSerProPheSerGlyAspGly 164
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 4644 GAAAACAGCCGAGAACGAAACACGAAACGAAACGAAACGAAACAAAGAGGC 4703

Qy 165 GinProPhelysAspIleProGlyLysGlyGluAlaThrGlyProAspLeuGluGlyLys 184
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 4704 -----AAAACCAGAGAAGGACAAACACGAAACAAAGAACAGAAAAA 4754

Qy 185 AspIleGln----- 187
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 4755 GAAAACAGGAAACCGGAAACACAGAGAACACAAACGAAACGAAACAAAGAAC 4814

Qy 188 -----ThrGlyPheAlaGlyProSerGluAlaGluSerThrHis 200
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

RESULT 2
 US-08-524-757-11
 Sequence 11, Application US/08524757
 ; Patent No. 5792634
 ; GENERAL INFORMATION:
 ; APPLICANT: Conaway, Ronald C.
 ; ADDRESS: Conaway, Joan W.
 ; TITLE OF INVENTION: RNA Polymerase Transcription Factor
 ; NUMBER OF SEQUENCES: 37
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: RICHARDS, MEDLOCK & ANDREWS
 ; STREET: 1201 Elm Street, Suite 4500
 ; CITY: Dallas
 ; STATE: TX

COUNTRY: US
 ZIP: 75270-2197
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/524,757
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/13621
 FILING DATE: 29-NOV-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/160087
 FILING DATE: 30-NOV-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Harre, John A.
 REGISTRATION NUMBER: 37,345
 REFERENCE/DOCKET NUMBER: B35006CIPCTP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (214) 939-4500
 TELEFAX: (214) 939-4600
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2690 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: both
 FEATURE: CDS
 NAME/KEY: CDS
 LOCATION: 33...2351
 US-08-524-757-11

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
23	0.00039	140..00	32..08%	49		
660	0.00039	144..00	20..52%	144		
43	0.00039	6..14%	1..14%	17		

US-09-700-696C-2 (1-430) × US-08-524-757-11 (1-2690)

Qy 23 ProLySsThrGlyAsnLysGlyPheGluAspGlyAspAlaLeuSerlysLeuIle 42
 Db 660 CCTCGGAAAGGCCACGGCAATGCCATTGAGACTGGCCAGGCAAGAACGACAC 719

Qy 43 AspGlnGluGluGluTyrGlyAlaAlaLeuLeuArgAsnAsnMetGlnHisIleMetGlyPro 62
 Db 720 CRGGTrGAACCCCATGGAAAGGGTrGTGAGTCAAAAGAGCAC--- 767

Qy 63 ValThrAlaIleLeuLeuGlyGluGluAsnLysGluAsnThrProArgAsnValLeu 82
 Db 768 -----AATCTTCACAGGCAAAGCCCCTGTG 797

Qy 103 GlnArgAspSerGlnAlaGlnLysSerProValLysSerlysLeuIleSerlysLeuIle 122
 Db 798 GATGCCAAGATGATGAGAAAGGCCCTGTGTTGAGCAGAGAAATCAC 848

Qy 123 HisAsnIleAspTyrLeuLysHsIleLeuSerLysValLysSlysLeuProSerAspPheGlu 142
 Db 849 -----AAGGCCCTTCACAA----- 863

Qy 143 GlySerGlyTyrThrAspLeuGluArgGlyAspAsnAspIleSerProPheSerGly 162
 Db 864 -----GAGGAAACCGAACGCCACCCTAGGG 890

RESULT 3
 US-07-814-964-10
 ; Sequence 10, Application US/07814964
 ; Patent No. 5,355047
 ; GENERAL INFORMATION:
 ; APPLICANT: Donahue, Brian A.
 ; APPLICANT: Toney, Jeffrey H.
 ; APPLICANT: Brinna, Suzanne L.
 ; APPLICANT: Pil, Peter M.
 ; APPLICANT: Brown, Steven
 ; APPLICANT: Kellett, Patti
 ; APPLICANT: Essigmann, John M.

APPLICANT: Lippard, Stephen J.

TITLE OF INVENTION: DNA Structure Specific Recognition Protein and Uses Therefor

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS: 13

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: 2 Miltont Drive

CITY: Lexington

STATE: MA

COUNTRY: USA

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/814, 964

FILING DATE: 19911226

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/539, 906

FILING DATE: 18-JUN-1990

ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia

REGISTRATION NUMBER: 32, 227

REFERENCE/DOCKET NUMBER: MIT-4787AAA

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-361-6240

TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 2384 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE:

ORGANISM: Drosophila melanogaster

IMMEDIATE SOURCE:

CLONE: Drosophila SSRP - composite sequence

POSITION IN GENOME/SEGMENT: 2

MAP POSITION: 60A 1-4

FEATURE: CDS

NAME/KEY: CDS

LOCATION: 123...2291

US-07-814-964-10

Alignment Scores:

Pred. No.:

Score: 0.000459

Length: 2384

Matches: 99

Conservative: 50

Mismatches: 136

Indels: 182

Gaps: 23

DB: 1

US-09-700-696c-2 (1-430) x US-07-814-964-10 (1-2384)

QY 16 GlyLeuArgMetSerIleTyrProLysSerThrGly-HisLysGlyPheGluAspGlyAs 35

DB 1187 GGAGCGAGATTCTATCCATAAGCCACCTGCAATTCGGCTTTGAGGAG 1241

QY 35 paspAlaIleSerLysLeuHisAspGlnGluGlyIleAla----- 49

DB 1242 -----ATTAGTCTGTGAACTTGTGAACTTGTGAACTTGTGAACTTGTGACTT 1294

QY 50 -----AlaLeuIleArgAspAsnMetGlnHisIleMetGlyProValThrAlaIleLysLe 68

DB 1295 CGAAGTGAGCTCAAAGCACTGTTCACTATCCTCCATAGACGGAGCGCTTC 1340

QY 68 uLeuGlyGluGluAsnLysGluAsnThrProArgAsnValLeuAsnIleProAlaSe 88

DB 2057 TCCATCCAGAACGGCGATAACCTGGGAGCTCAGAGCAAGGAGTACATTTCGA 2116

	Db	1341	-----GAGAGGGAGG-----	1352
	Qy	88	rMetAsnTyAlaLysAlaIleSerLysAspLysLysProGlnArgAspSerGlnAl	108
	Db	1353	-----TATGCCAAGCTC	1364
	Qy	108	aGlnIysSer-ProValLySerSerThrHisArgIleGlnHiAsnIleAspIysLysLe 128	
	Db	1365	-----TTCGACATAC	1375
	Qy	128	uLys-----HisLeuSerLysValLysLysIleProSerAspPheGluGlySe 144	
	Db	1376	CACACGAAAGAGTTCATCTCAGAAACATGGCCAG-----GCAAGAG	1420
	Qy	144	rgLYTYrThnAspLeuGlnGluArgIysAspAsnIleSerProHeSerGlyAspG1	164
	Db	1421	CGGCTPACAGGACTG-----GACTTTGTGATTGCA	
	Qy	164	yGlnProphelyAspIleProGly-----LysGlyLysAlaThrGlyProAspLeuGluGl 183	
	Db	1463	CGAACAGATGGCTPATCTGGCTCAAGGCTAGCCAGAAAGGAGGAGCA	1522
	Qy	183	yLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHisLeuAspR	203
	Db	1523	CGACCAT-----GCGACTCCGATGAGAGTGCACCGTACGACGACT	1564
	Qy	203	rLysLysProGlyTyAsnGluIleProGluAfgLysGluAsnGlyLysAsnThrIleG1	223
	Db	1565	C--AAGCCAAACGAGAACGAGTCGGTGGCCAGGGTATGACGAGAACGTCAGTGAGGAG 1621	
	Qy	223	yThrArgAspPglUralysGluAlaAspAlaValGluGlyLysGly 243	
	Db	1622	TGATTCGGAGAT-----GACGACATGCTAGTAGTGGC-----GCGGG 1657	
	Qy	243	rAsnAspIleMetGlySerThrAsnPhenylsGluLeuProGlyArgGluGlyAsnArgV 263	
	Db	1658	AGGCCAACGGACCGCCAGAAAAAGAGGAGAAACTCCGAGAACTGAGCAAGAAAGCAAAA 1717	
	Qy	263	IaspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPhenylsTyrProProAlaPr 283	
	Db	1718	GGAGAAAACACAGGAGAACGACTCTGGGAAACCCAAGCCGCOACCAACCGGTTCACTGCTCTG 1816	
	Qy	283	oSerIysGluIleArgLysGluIysSer-----AAACC 1756	
	Db	1757	CTCCAGAACGAGAACGACTCTGGGAAACCCAAGCCGCOACCAACCGGTTCACTGCTCTG 1816	
	Qy	293	-----SerAspAlaAlaGluSer-----ThrAsnTyAsnGluI	304
	Db	1817	GCTGAAGCACGCGCGAGCATCAAGGCTAAAGGCTTACCGGAGAT 1876	
	Qy	304	eProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAspArgAsnGlnAl 324	
	Db	1877	CGCCAGAAAGGGCCGGAGATGTCGAAGGAGCTGAAAGCAAGTCCAAAGTGGAGGATG 1936	
	Qy	324	athrLeuAsnGluIysGlnArgPheProSerLysGlyLysSerGlnGlyLeuProIlePr 344	
	Db	1937	GGGGCAGAACGAGAACGAGCGCTAC-----	1961
	Qy	344	oSerArgGlyLeuAsnGluIleArgLysTyrHistYValProHisArgGlnAsnAsnSe 384	
	Db	1962	-----CAGCAGGAGATCGCAACTAAAGCTGAAAGGGGGGGGTGACAG 2005	
	Qy	384	rThrArgAsnLysGlyMetProGlnGlyLysGlySerItpGlyArg-----GlnProH 402	
	Db	2006	CGAACGAGAACGGGT-----GAAAGTCCTCCAGAACGGAGCGAGCGCTTC 2056	
	Qy	402	sSerAsnArgArg-----PheSerArgArg-----ArgAs 413	
	Db	2057	TCCATCCAGAACGGCGATAACCTGGGAGCTCAGAGCAAGGAGTACATTTCGA 2116	

Qy 413 PAspSerSerGluSerSerAspSerGlySerSerGlu----- 426
 Db 2117 CGAGACTTACCACTTCGAGCAGAGAACGAGCTGCCAAGAAGAGAGCA 2176

Qy 427 -----SerAspGlyAsp 430
 Db 2117 GCCCCATCGACGCGCAT 2195

RESULT 4
 US-08-258-442-10
 Sequence 10. Application US/08258442
 Patent No. 5,670,521

GENERAL INFORMATION:

APPLICANT: Donahue, Brian A.
 APPLICANT: Toney, Jeffrey H.
 APPLICANT: Bruhn, Suzanne L.
 APPLICANT: Pil, Pieter M.
 APPLICANT: Brown, Steven
 APPLICANT: Kellef, Patti
 APPLICANT: Essigmann, John M.
 APPLICANT: Lippard, Stephen J.

TITLE OF INVENTION: DNA Structure Specific Recognition
 TITLE OF INVENTION: Protein and Uses Therefor
 NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 STREET: 2 Millitile Drive
 CITY: Lexington
 STATE: MA
 COUNTRY: USA
 ZIP: 02173

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/258,442
 FILING DATE:
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/539,906
 FILING DATE: 18-JUN-1990
 ATTENDEE/AGENT INFORMATION:
 NAME: Granahan, Patricia
 REGISTRATION NUMBER: 32,227
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-861-6240
 TELEFAX: 617-861-9540
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2,384 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 ORIGINAL SOURCE:
 ORGANISM: Drosophila melanogaster
 IMMEDIATE SOURCE:
 CLONE: Drosophila SSRP - composite sequence
 POSITION IN GENOME:
 CHROMOSOME/SEGMENT: 2
 MAP POSITION: 60A 1-4
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 123...2291

US-08-258-442-10

Alignment Scores:
 Pred. No.: 0.000459
 Score: 138.50

Percent Similarity: 31.91%
 Best Local Similarity: 21.20%
 Query Match: 6.08%
 DB: 1
 Gaps: 23

Percent Similarity: 31.91%
 Best Local Similarity: 21.20%
 Query Match: 6.08%
 DB: 1
 Gaps: 23

US-09-700-696C-2 (1-430) x US-08-258-442-10 (1-2384)

Qy 16 GlyLeuArgMetSerIleTerProLysSerThrGlyAsnLysGlyPheGluAspGlyAs 35
 Db 1187 GGAGGAGGATTCTATCCAAAGCCACGGTGCATATCCCCTTGAGGAG---- 1241
 Qy 35 PAspAlaIleSerIysLeuHisAspGlnGluGlyGlyAla---- 49
 Db 1242 -----ATTAAGTTCTGTGAACTTGAACTTGCCGATCTCCACGCGGATCCACGGGATTCGACTT 1294
 Qy 50 -----AlaLeuIleArgAsnAsnTerAlaIleSerIysLeuHisAspGlyProAlaIleLysIle 68
 Db 1295 CGAAAGTGAGGCTCAAGAACGGAACACTTACATCTCTCCACAC---- 1340
 Qy 68 uLeuCgIyGluGluAsnLysGluAsnThrProArgAsnValLeuAsnIleProAlaAs 88
 Db 1341 -----GAGAGGGAGAG---- 1352
 Qy 88 rMetAsnTyraIalysAlaHisSerLysAspLysLysProGlnArgAspSerGlnAl 108
 Db 1353 -----TATGCCAAGCTC---- 1364
 Qy 108 aGlnIysSerProValLysSerTerThrHisArgIleGlnHisAsnIleAspTerIle 128
 Db 1365 -----TTCGAATCAT 1375
 Qy 128 uLys-----HisLeuSerLysValLysIleProSerAspPheGluGlySe 144
 Db 1376 CACACAGAGAAAGTGTGAVTCGCAACATGGCAAG---- 1420
 Qy 144 rGlyTyrrAspIleGlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspG1 164
 Db 1421 CGGTACACAGGACGTG----GACTTGGGATTCGGAC---- 1462
 Qy 164 yGlnProIleAspIleProGly-----DysGlyIleAlaThrIleProAspIleGluGlu 183
 Db 1463 CGAACACATGCCTATCGGCTCGCTCAGGTGAGGGAGGAAACGGGAGGAGCA 1522
 Qy 183 yLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHisLeuAspTh 203
 Db 1523 CGGTGAT-----GGGACTCGGATGAGACTCACCGATAAGGACTT 1564
 Qy 203 rLysLysProGlyTyrrAsnGluIleProGluArgGluGluAsnGlyGlyAsnThrIleG1 223
 Db 1565 C--AAGCCCAAACGAGACGAGTCCGATGTCGGAGAGATGACACCAAACCTGGAGAG 1621
 Qy 223 yThrArgAspGluIleAspIleAlaLysIleIleAspIleValGluGlySe 243
 Db 1622 TGATTGGGACGAT-----GACAGGATGCTGAGTCGCGC-----GGCG 1657
 Qy 243 rAsnAspIleMetGlySerIleAspIleAspIleValGluGlyAsnArgVa 263
 Db 1658 AGGCGAACGCCAGGCCAGAACGAAAGAAGAAGAAGTCGAGTCGAGAAAGGAAA 1717
 Qy 263 IAspAlaIleSerGlnAsnAlaHisGlnGlyLysValGluPheHistYrrProAlaPr 283
 Db 1718 GGAGAAAACACAAAGGAAAGGACAAGAACGAAAGGACAAG-----AAACC 1756
 Qy 283 oserIysGlySerIysGlyGlySer----- 292
 Db 1757 CTCCAAAGAGAAAGGAACTCTGGCAAAACCCAAAGGGGCCACACCGCTTCATGCTCTG 1816
 Qy 293 ---SerAspAlaAlaIleUser-----ThrAsnTyrAsnGluI 304
 Db 1817 GCTGAACAGCCAGGCCAGAGATCAGAGTCAGAGTCAGGATCCGGCAT 1876
 Qy 304 eProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsnArgAsnGlnAl 324

Db 1877 CGCAAGAAGGGCGGCGAGATGGAGGAGTGAAGCAGTCAGGGAGGATGC 1936
 Qy 324 athrIeuAsnGluLysGlnArgPheProSerLysGlySerGlnGlyLeuProfilePr 344
 Db 1937 GCGGCCAGACAAGGACCTAC----- 1961
 Qy 344 oSerArgGlyLeuAspAsnGluMetAspSerPheAsnGlyProSerSerHi 364
 Db 1961 -----
 Qy 364 sGluAsnIleIleThrHisGlyArgLysThrIstYrValProHisArgGlnAspAsnSe 384
 Db 1962 -----CA CGCGAGATGCGGAACTAAGCTGAAGCGGGGGTGACAG 2005
 Qy 384 rThrArgAsnLysGlyMetProGlnGlyLysSerIrpGlyArg----GlnProHi 402
 Db 2006 CGACAAAGGAGGGT-----GAAAGTCCTCAAGAGCGAAAGACGGAGCCTC 2056
 Qy 402 sSerAsnArgArg-----PheSerSerArgArg-----ArgAs 413
 Db 2057 TCCATCCAGGCGAAATACTGGCGAGCTCAAGGAGTACATTTCGGA 2116
 Qy 413 pAspSerSerGluSerSerAspSerSerGlySerSerGlu----- 426
 Db 2117 CGACGACTTACCAAGCTCGAGCACAGAACGAGCTGCCAAAGAAAGGCCA 2176
 Qy 427 -----SerAspGlyAsp 430
 Db 2177 GCCCCCCATCCGACGGGT 2195

RESULT 5

Sequence 5, Application US/08328809
Patent No. 5705334

GENERAL INFORMATION:

- APPLICANT: Lippard, Stephen J.
- APPLICANT: Bissmann, John M.
- APPLICANT: Donahue, Brian A.
- APPLICANT: Toney, Jeffrey H.
- APPLICANT: Bruhn, Suzanne L.
- APPLICANT: Pil, Pieter M.
- APPLICANT: Brown, Steven
- APPLICANT: Rellett, Patti

TITLE OF INVENTION: Uses For DNA Structure-Specific
TITLE OF INVENTION: Recognition Proteins

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Patent Administrator, Testa, Hurwitz & Thibault
STREET: 53 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328, 809
FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

- NAME: Fenton, Gillian M.
- REGISTRATION NUMBER: 36, 508
- REFERENCE/DOCKET NUMBER: MIT-023 (5473/24)
- TELEPHONE: 617-248-7000

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

- LENGTH: 2384 base pairs
- TYPE: nucleic acid

Db 106 STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Drosophila melanogaster
IMMEDIATE SOURCE:
CLONE: Drosophila SSRP - composite sequence
POSITION IN GENOME:
CHROMOSOME SEGMENT: 2
MAP POSITION: 60A 1-2
FEATURE:
NAME/KEY: CDS
LOCATION: 123..2291

Db 118 Alignment Scores:
Score: 0.000459
Percent Similarity: 138.50
Best Local Similarity: 31.91%
Query Match: 6.08%
DB: 1
Length: 2384
Matches: 99
Conservative: 50
Mismatch: 136
Ends: 182
Gaps: 23

US-09-700-696C-2 (1-430) x US-08-328-809-5 (1-2384)

Qy 16 GlyLeuArgMetSerIleThrProltyrProLysSerThrGly-AbsnLysGlyPheGluAspGlyAs 35
Db 1187 GGAGCAGGGATTCACTATATCCAAAGCCACCGGATCATCCGTTGAGG----- 1244

Qy 35 PASpAlaIleSerlysIleHisAspGlnGluGlyLysGlyAla----- 49
Db 1242 -----ATTAGTTGTGACTTTCGACTTTCGACTTCATCTCTCCATC----- 1299
Qy 50 -----AlaLeuIleArgAsnAsnMetGlnHisIleMetGlyProValThrAlaIleLysLe 68
Db 1295 CGAAAGTGACGCTCAAGAACTGGAAACTGTTCAACATCTCTCCATC----- 1344
Qy 68 uLeuDglyGluGluLysLysIleAsnThrProArgAsnValLeuAsnIleIleProAlaLe 88
Db 1341 -----GAGAGGAGGAG----- 1356
Qy 88 rMetAsnTyrAlaIleSerIleAsnSerGlyAspSerGlnAl 108
Db 1353 -----TATGCCAAGCTC----- 1366
Qy 108 aGlnIleSerProValIleSerIleAsnSerGlyAspSerGlnAl 128
Db 1365 -----TTCGACTACAT 1375
Qy 128 uLys-----HisLeuSerLysValLysIleProSerAspPheGluGlySe 144
Db 1376 CACACAGAAAGTGGCAGTGGCAACATGGCAAG-----GCAAGAGG 1420

Qy 144 rGlyTyrrAspIleGlnGluArgGlyAspAsnAspIleSerProHeSerGlyAspGly 164
Db 1421 CGCTACAGGACCTG-----GACTTGGGATTCGAC-----AAGAGAGA 1462

Qy 164 yGlnProHeLysAspIleProGly-----LysGlyGluIalaThrGlyProAspIleGluGly 183
Db 1463 CGAACTAGATGCCATGCTCAGCTGAGGAGGAAACGAGGAGGAGCA 1522

Qy 183 yLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHisLeuAspIle 203
Db 1523 CGAGAT-----GGGACTCAGGGATGAAGAGTCACGGATGAGGACTT 1564

Qy 203 rLysLysProGlyTyAsnGluIleProGluLargGluArgGluAsnGlyAsnThrIleG 223
Db 1565 C-----AAGGCCAAAGGAACTGGAGATGACGCCAATGGAGAG 1621

Qy 223 yThrArgAspGlutIalaLysGluAlaAspAlaValAspValSerLeuValGluGlySe 243
Db 1622 TGATTGGACAT-----GACAGGATGCTATGTCG-----GGCG 1657

QY 243 rAsnAspIleMetGlySerThrAsnPheLysGluIleProGlyArgGluGlyAsnArg 263
Db 1658 AGGGACACCGAACGCCAAGAAAAAGAGGAGAAAGTCCGAGAAAAGAA 1717 :::::
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/866,840
; FILING DATE: 02-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Panton, Gillian M.
; REGISTRATION NUMBER: 36,108
; REFERENCE/DOCKET NUMBER: MIT-023 (5473/24)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7100
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2384 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE: Drosophila melanogaster
; IMMEDIATE SOURCE:
; CLONE: Drosophila SSR - composite sequence
; POSITION IN GENOME:
; CHROMOSOME SEGMENT: 2
; MAP POSITION: 60A 1-4
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 123..2291
; US-08-866-840-5
; Alignment Scores:
; Pred. No.: 0.000459 Length: 2384
; Score: 138.50 Matches: 99
; Percent Similarity: 31.91% Conservative: 50
; Best Local Similarity: 21.20% Mismatches: 136
; Query Match: 6.08% Indels: 182
; DB: 4 Gaps: 23
; US-09-700-696C-2 (1-430) x US-08-866-840-5 (1-2384)
QY 16 GlyLeuArgMetSerIleTyrProLyserThrGly-AsnLysGlyPheGluAspGlyAs 35
Db 1187 GGAGCGGAGATCATATATCACAGCCACGGTTGAGAT 1241 :::::
; PASPAAlleSerLysLeuHisArgInGluLysTyrGlyAla--:::|:|||:|||:|||:|||:
QY 35 PASPAAlleSerLysLeuHisArgInGluLysTyrGlyAla--:::|:|||:|||:|||:|||:
Db 1242 ---ATTAGTCCTGTAACTTGCCGAGGGATCCAGGGATCTTCGACTT 1294 :::::
; 50 ---AlaLeuIleArgDnsABIMetGlnHistLeMgIyProValThrAlaLysLe 68 :::
Db 1295 CGAAGTGAAGCTCAAGAACGAACTGTCACTCTCTCCATC----- 1340 :::
; 68 uIeuglyIgluGluAspLysGluAsnThrProArgAsnValLeAsnIleProAlaSe 88 :::
Db 1341 -----GAGAACGGGG----- 1352 :::
; 88 rMetAsnTrpAlaHisSerLysAspLysLysProGlnArgAspSerGlnAl 108 :::
Db 1353 -----TATGCCAACCTC----- 1364 :::
; 108 aGlnLysSerProValLysSerThrArgIleAspTyrLe 128 :::::
Db 1365 -----HisIleSerLysValLysIleProSerAspPheGlucIySe 1375 :::
; RESULT 6
; US-08-866-840-5
; Sequence 5, Application US/08866840
; Patent No. 6475791
; GENERAL INFORMATION:
; APPLICANT: Lippard, Stephen J.
; APPLICANT: Essigmann, John M.
; APPLICANT: Donahue, Brian A.
; APPLICANT: Toney, Jeffrey H.
; APPLICANT: Bruhn, Suzanne L.
; APPLICANT: Pil, Pieter M.
; APPLICANT: Brown, Steven
; APPLICANT: Kellelt, Patti
; TITLE OF INVENTION: Uses For DNA Structure-Specific
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Administrator, Testa, Hurwitz & Thibeault
; STREET: 53 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; 144 rGlyTyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPheserGlyAspG1 164 :::::

1421 CGCTATAAGACGTG --GAATTGGTATTGGAC-----AACGAA 1462
 164 yGlnProPheLysAspIleProGly--LysGlyGluAlaThrGlyProAspLeuGluG1 183
 1463 CGAACCATGCCATCTGGCTGCGCTCAAGCTGAGCGAGGAAAGGAGGAGCA 1522
 183 yLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrIleLeuAspPhe 203
 1523 CGACAT-----GGCAGCTGGATGAAAGTCACGAGTGGAGAACT 1564
 203 rLysLysProGlyTyrosGluLysGluProGluArgGluGluAsnGlyGlyAsnThrIleG1 223
 1565 C---AAGCCAAAGGAGAACGAGTCGCGTGGCGAGGAATGACGAACTGGAGAG 1621
 223 yThrArgAspGluThrAlaLysGluAlaSpIleValGluGly 243
 1622 TGATTCGAGCGAT-----GACGGATGCTAGTGC 1657
 243 rAsnAspIleMetGlySerThrAsnPhenylGluLeuProGlyArgGluGlyAsnArgVa 263
 1656 AGGGACACGACGCGAACAGGAAAGGAAAGAAGTCGAGAGAAAGAGANAAA 1717
 263 1ASDAlaGlySerGlnAsnAlaLahisGlnGlyIysValGluPheHisTyrProProAlaPr 283
 1718 GGAAAAPAAPACACAGGACAAAGGAGAACAAARG-----AAAC 1756
 283 oSerLysGluLysArgLysGluGlySer----- 292
 1757 CTCCAAGAAGAAAGGAGACTCTGCCAAACCCAAAGGGCACCACCGCTTCATGCTCTG 1816
 293 ---SerAlaAlaGluSer-----ThrAsnTyAsnGluI 304
 1817 GCTGAAACGACACGGCGGAGCATCAAGGGAAATCGGGCATAAAGGTTACCGAGAT 1876
 304 eProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsnArgAsnGlnA1 324
 1877 CGCCAAAGAAGGGCGGCGGAGATGTAAGGAGCTGAAGTCGAGTGAGGATG 1936
 324 aThrLeuAsnGluLysGlnDargPheProSerLysGlyLeuProIlePr 344
 1937 GGCGCCAAAGCACAGCACGCTAC----- 1961
 344 oSerArgGlyLeuAspIleSerGluIleLysAsnGluMetAspSerPheAsnGlyProSerH1 364
 1961 ----- 1961
 364 sGluAsnIleIleThrHisGlyArgLysTyrHistYValProHisArgGlnAsnAsnSe 384
 1962 -----CAGACGAGATGGCAACTACAGGCCAAAGCCCCGCGTGATAG 2005
 384 rThrArgAsnLysGlyMetProGlnGlyLysGlySerItpGlyArg-----GlnProH1 402
 2006 CGACACGAGAGGT-----GGAAGTCTCCAGAAAGGGCAAACAGGAGCCTC 2056
 402 sSerAsnAspArg-----PheSerSerArg-----ArgA 413
 2057 TCCATCAAGAAGGGCAAATACCTCGGACGGGTTCAAGAGCAAGGAGTACATTTCGA 2116
 413 PaspSerSerGluSerSerAspSerGlySerSerGlu----- 426
 2117 CGACACTTCAACAGCTTCAAGGAGAAGGACAAGGAGGAGGAGCA 2176
 427 -----SerAspGlyAsp 430
 2117 GCCCCCCATCCGAGGGCAT 2195

RESULT 7
 PCT-US92-11107-10
 Sequence 10, Application PC/TUS9211107
 GENERAL INFORMATION:
 APPLICANT: Donahue, Brian A.
 APPLICANT: Toney, Jeffrey H.
 APPLICANT: Bruhn, Suzanne L.
 APPLICANT: Bruhn, Pieter M.
 APPLICANT: Brown, Steven
 APPLICANT: Kellelt, Patti
 APPLICANT: Bessigmann, John M.
 APPLICANT: Lipppard, Stephen J.
 TITLE OF INVENTION: DNA Structure Specific Recognition
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 STREET: 2 Militia Drive
 CITY: Lexington
 STATE: MA
 COUNTRY: USA
 ZIP: 02173
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/11107
 FILING DATE: 1992/12/18
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/539, 906
 FILING DATE: 18-JUN-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Granahan, Patricia
 REGISTRATION NUMBER: 32, 227
 REFERENCE/DOCKET NUMBER: MIT-4787AA
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-861-6240
 TELEX/FAX: 617-861-9540
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2384 base pairs
 TYPE: NUCLEAR ACID
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 ORIGINAL SOURCE:
 ORGANISM: Drosophila melanogaster
 IMMEDIATE SOURCE:
 CLONE: Drosophila SSRP - composite sequence
 POSITION IN GENOME:
 CHROMOSOME/SEGMENT: 2
 MAP POSITION: 60A 1-4
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 123..2291
 PCT-US92-11107-10

Alignment Scores:
 Pct. No.: 0.000459
 Score: 138.50
 Percent Similarity: 31.91%
 Best Local Similarity: 21.20%
 Query Match: 6.08%
 DB: 5
 Gaps: 23

US-09-700-696C-2 (1-430) x PCT-US92-11107-10 (1-2384)
 QY 16 GlyLeuArgMetSerIleTyrProLysSerThrGlyAsnLysGlyPheGluAspGlyAs 35
 Db 1187 GGAGCAGGATTCACTATATCCACAGCCGATCATCGCTTGGAG----- 1241
 QY 35 PAPALaleSerIleLysLeuIleAspGlnGluIleUtyGlyAla----- 49
 Db 1242 -----ATTAGCTCTGAACTTTCGGCAACGGGATCCACGGGATCTTCGACTT 1294
 QY 50 -----AlaLeuIleArgAsnAsnMetGlyProValThrAlaLeuIleMetGlyProValThrAlaLeuIle 68

Db 1295 CGAAGTGAAGCTCAAAGGAACTGGTACATCTTCATCCATC----- 1340
 Qy 68 uLeuGlyLysSerAsnThrProArgAsnValLeuAsnIleLeuProAlaSe 88
 Db 1341 -----GAGAACGGAGG----- 1352
 Qy 88 rMetAsnTyrrAlaLysSerLysAspLysLysProGlnArgAspSerGlnA 108
 Db 1353 -----TATGCCAAAGCTC-----
 Qy 108 aGlnLysserProValLysSerLysAspLysLysProGlnArgAspSerGlnA 1364
 Db 1365 -----
 Qy 128 uLys-----HiLeuSerLysValLysLysProSerAspPheGluGlySe 144
 Db 1376 CACACAGAAGTTGCAATGGCACATGGCAAG-----GCAAGAGG 1420
 Qy 144 rGlyTyrThrAspLeuGluArgGlyAspAsnAspIleSerProPheSerGlyAspGly 164
 Db 1421 CGCTTAAGGAGCTG-----GACTTGATGATCGAC-----AACGAGA 1462
 Qy 164 yGlnProPheLysAspIleProGly---LysGlyGluAlaThrGlyProAspLeuGluGly 183
 Db 1463 CGAACCAATGCTCATATGGCTCGCTCAAGAATGCTGAGGGAAAGGAGGACCA 1522
 Qy 183 yLysAspIleGlnThrGlyPheAlaGlyPrSerGluAlaGluSerThrHisLeuAspTh 203
 Db 1523 CGACGAT-----GGCAGACTCGGATGAGGTCCACGGATGAGGACTT 1564
 Qy 203 rLysLysProGlyTyrAsnGluLysGluAsnGlyLysAsnThrIleGly 223
 Db 1565 C-----AAGCCCCAACGAGAACGAGTCGGATGTCGGCGGGAGTATGACAGGCAACGTCGAGAG 1621
 Qy 223 yThrArgAspGluThrAlaLysGluLaaAspAlaValAspValSerLeuValGluGlySe 243
 Db 1622 TGATTTCGACGAT-----GACCGCATGCTAATGGC-----
 Qy 243 rAsnAspIleMetGlySerThrAsnPheLysGluLeuProGlyArgGluGlyAspArgY 263
 Db 1628 AGCGCAGCGGCAAGGCCAAAGAAAGAAAGAAAGAAAGAAAAAA 1717
 Qy 263 LAspAlaGlySerGlnAlaHiSglnglyLysValGluPheHistYPrProAlaPi 283
 Db 1718 GGAAA AAAACACAAGGAAAGGAGAACAAAG-----AAACC 1756
 Qy 283 oserLysGluLysArgLysGluGlySer-----
 Db 1757 CTCCAAGAAGAACGACTGGCAAACCCAAAGCGGCCACCGCTTCATGCTCTG 1816
 Qy 293 ---SerAspAlaAlaLysSer-----ThrAspTyrAsnGluL 304
 Db 1817 GCTGAACACACGGCGAGATCAAGGAAAMATCGGGCATAAAGGTTACCGAGT 1876
 Qy 304 eProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAspGlnAl 324
 Db 1877 CGCAAAAGGCGGGCAAGATGTGAGTGANAGCAAGTGGAGGATGC 1936
 Qy 344 oserArgGlyLeuAspAsnGluLysAsnGluMetAspSerPheAsnGlyProSerHi 364
 Db 1961 ----- 1961
 Qy 364 sGluAsnIleLeuThrHisGlyArgLysSerThrArgLysGluAsnAsnSe 384
 Db 1962 -----GAGGACGAGATGCGCAACTACAGCTGAGCGGGGGTGACAG 2005
 Qy 384 rThrArgAsnLysGlySerGlyNetProdLysGlySerGlyArg-----GlnProHi 402
 Db 2006 CGCAAAACGAAAGGGT-----GCAAGTCTCCAAAGAGGCGAAAGACGGAGCTTC 2056

Qy 402 sSerAsnArgArg-----ArgAs 413
 Db 2057 TCCATCCAGAAGGGCAATACTCGGCAAGGGCTCAAGGCCAAGGATCATTCGG 2116
 Qy 413 pAspSerGluSerAspSerGlySerSerGlu----- 426
 Db 2117 CGGACTCCACAGTCGACGACGAAAGAACGAGCTCAGGCCAAGAGGCAA 2176
 Qy 427 -----SerAspGlyAsp 430
 Db 2177 GCCCCATCGAACGGAT 2195

RESULT 8
 US-08-340-559-27
 Sequence 27, Application US/08320559
 ; Patent No. 5633135
 ; GENERAL INFORMATION:
 ; APPLICANT: Croce, Carlo
 ; APPLICANT: Cananei, Eli
 ; TITLE OF INVENTION: Diagnostics, Therapeutics and Methods for
 ; TITLE OF INVENTION: Detection and Treatment of Acute Leukemias
 ; TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the
 ; TITLE OF INVENTION: All-1 Region
 ; NUMBER OF SEQUENCES: 44
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5633135ris
 ; STREET: One Liberty Place - 46th Floor
 ; CITY: Philadelphia
 ; STATE: PA
 ; ZIP: 19103
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: WORDPERFECT 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/320,559
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/062,443
 ; FILING DATE: 14 MAY 1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/971,094
 ; FILING DATE: 30-OCT-92
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/888,830
 ; FILING DATE: 27-MAY-92
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/805,093
 ; FILING DATE: 11-DEC-91
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: DeLuca, Mark
 ; REGISTRATION NUMBER: 33,229
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (215) 568-3100
 ; TELEFAX: (215) 568-3439
 ; INFORMATION FOR SEQ ID NO: 27;
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 9370 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 469..4032
 ; US-08-320-559-27
 Alignment Scores:

Pred. No.: 0.00499 Length: 9370 Qy 311 SerThrArgLysGlyValAlaSpHissSerAsnArgAsnAlaThrLeuAsnGluLysGln 330
 Score: 137.00 Matches: 100 Db 2848 GAAGCAGAAAGATGTGAT-----AAGAGAAATC 2880
 Percent Similarity: 34.70% Conservative: 61 Qy 331 ArgPheProSerLysGlyLeuProSerArgGlyLeuAspAsn 350
 Best Local Similarity: 21.55% Mismatches: 192 Db 2881 AGA-----CTGGAGAAG 2892
 Query Match: 6.01% Indels: 113
 DB: 1 Gaps: 17

US-09-700-696C-2 (1-430) x US-08-320-559-27 (1-9370)

Qy 37 AlaIleSerLeuLeuIleAspGlnGluGlyIleAlaLeuIleArgAsnAsnMet 56 Qy 351 GluIleAsnGlnNetAspSerPheAsnGlyProSerHisGluAsnIleIleThr--- 369
 Db 1938 GCAGCTGGACAACTGCTGACCAAGTCAGCCAGGTCGCCAACAGGGCCCCAG 1997 Qy 351 GluIleAsnGlnNetAspSerPheAsnGlyProSerHisGluAsnIleIleThr--- 369
 Db 2055 GAGTC-AGGACCATTCGAATCCAAGATCTCCCG-----CTAAAAGCT 2098 Db 2893 GAATCAAATCACGTCATCTCATCTCACACTTCACAGTCTAACAAAGATAAG 2952
 Qy 57 GlnHisIleMetGlyProValThrAlaIleIleLeuLeuGlyGluIleAsnGluAsn 76 Qy 370 -----HisGlyArgLysThrIstYrValProHisArgGlnAsn 382
 Db 1998 GAGCAC-AGAGCCCACACGGGACCCAGAGTAGGCGAGAGCTGACAGTGCCAC 2044 Db 2953 CCCTCAGGGCCCTCTCACAGTCTAACAGGAAATGCTCCCCGCCACCGGTGTC 3012
 Qy 77 ThrProArgAsnValLeuAsn-----IleIleProAlaSerMetAsnTyraLeuAsn 94 Qy 383 AsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySer----- 396
 Db 2009 CC-AGGAAAGCCGCCACCCGGGCCACCCGGAAAGGGAGCTGTCAG 2157 Db 3013 TCGTCTCCCGAAAGCAGCCAAAGGGAAAGCAGACACC 3072
 Qy 95 HisSerLysAspLysSerLysProGlnArg-----AspSerGlnIleArg 109 Qy 397 TrpGlyArgGlnPro----- 409
 Db 2158 AAAGTCTCCGGCACAGGAAACCCCCAACGGAAACCTTGGAACCAAACCCAA 2217 Db 3073 TGTGGCCGACCCCTCCCAAAAGTCCAGGAGTACCAAGGCCAACACAAAGCTTC 3132
 Qy 110 LysSerProValLysSerThrHisArgIleGlnHisAsnIleAspTyrlleIys 129 Qy 410 ArgArgArgAspSerSerAspSerGlySerSerGlySerSerGlySer----- 426
 Db 2218 -----AACCTGTCAAGGCCCTCTGCCGGCGAGGTCAACGCCACGGCTG 2262 Db 3133 ATTCCCAAGGAGAGAGAGTAGAGGAAAGGGCTCTGGGACACAGGGT 3192
 Qy 150 GlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspGlyGlnProPheLysAsp 169
 Db 2263 CAGGGAAAGGGCAGGCCGCTCTCCCTATGGCTCCGGAGAACAGACTCCAAAGAC 2322
 Qy 170 IlePro-----GlyLysGlyGlu----- 175
 Db 2323 AAGGCCAAAGGTGAAGGAAAGGGCGCCGGCGCACGAAGCAACCCAAAGCCA 2382
 Qy 176 AlaThrGlyProAspIleLeuGlyLysAspIleGlnThrIlePheAlaIleGlyProSerGlu 195
 Db 2383 GCAGTGGCCCCCTCTCCTAGTGGAGAAGAACACAGGCTCCCTCTGAAG 2442
 Qy 196 AlaGluSer-----ThrHisIleAspThrIleLysProGlyTyr--- 208
 Db 2443 GCTCTCTCAGGCCAGAACCCGAGGACAGCAGCCCTGACACTTT 2502
 Qy 209 -----AsnGluIleProGluArgGluGluAsnGlyGlyAsnThr 221
 Db 2503 GCTCTGTCTCCCTGACTGAGGCCACCCCAAGTGGCAGGCCAGGAGCT 2562
 Qy 222 IleGlyThrArgAspGluThrAlaLysGluAlaSpAlaValAspValSerLeuValGlu 241
 Db 2563 AGTGCCTGGCCCAAGGGCTGGTCTCCAGGACAGCCGAAAGACGACTCCCATG 2622
 Qy 242 GlySerAspAspIleMetGlySerThrAnPhenylsGluLeuProGlyIargGluGlyAsn 261
 Db 2623 CCTTGAGAACATCACCTGACTGAGGCCACCCCAAGTGGCAGGCCAGGAGCT 2682
 Qy 262 ArgVal-----AspAlaGlySerGlnAsnAla 270
 Db 2683 ATGGTGAAGATCACCTGACTGCTCTCAGGCTCAGGCAACTCTCCCGAAGGGAC 2742
 Qy 271 HisGlnGlyLysValGluPheHisTyrProProAlaProSerLysGluLysGlu 290
 Db 2743 CGCCAGGAAAGATAAACAGCCGCCAGGAAAGAACAGCTGAGAAG 2802
 Qy 291 GlySerSerAspAlaAlaGluSerThrAsnTyrasnGlyLysGly 310
 Db 2803 AGGAGCTGAGACGCTCA-----AGCAAGTTGGCCAAAGAGAAAGGGT 2847
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US-08/545,860
 ; FILING DATE: 07-MAR-1996
 ; CLASSIFICATION: 435
 ; PRIORITY APPLICATION DATA: PCT/US94/04496
 ; APPLICATION NUMBER: PCT/US94/04496
 ; FILING DATE: 22-APR-1994
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US92/10930
 ; FILING DATE: 09-DEC-1992
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/327,392
 ; FILING DATE: 19-OCT-1994
 ; APPLICATION NUMBER: US 08/320,559
 ; FILING DATE: 11-OCT-1994
 ; PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/062, 443
 FILING DATE: 14-MAY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/971, 094
 FILING DATE: 30-OCT-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/888, 839
 FILING DATE: 27-MAY-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/805, 093
 FILING DATE: 11-DEC-1991
 ATTORNEY INFORMATION:
 NAME: DeLuca, Esq., Mark
 REGISTRATION NUMBER: 33, 2229
 REFERENCE/DOCKET NUMBER: TUU-1262
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-3100
 TELEFAX: (215) 568-3439
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9370 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 469..4032
 US-08-545-860D-27
 US-09-700-696C-2 (1-430) x US-08-545-860D-27 (1-9370)

Alignment Scores:
 Pred. No.: 0.00499
 Score: 137.00
 Percent Similarity: 34.70%
 Best Local Similarity: 21.55%
 Query Match: 6.01%
 DB: 3
 DB: 17

Qy 37 AlaIleSerLysLeuHisAspGlnGluLysGlyAlaAlaLeuIleArgAsnAsnMet 56
 Db 1938 GAGGCTGGACACTGGTGAAGTCAGCCAGCTGGCCAGCTGGCCACCCAGGCCAG 1997

Qy 57 GlnHistLeuMetGlyProValThrAlaIleLysLeuLeuGlyGluGluAsnLysGluAsn 76
 Db 1998 GAGGCAC---AGAGCCCCAACGGCCACCCGAGTAAGGCGAGCAGTGCCAC 2054

Qy 77 ThrProArgAsnValLeuAsn-----IleIleProAlaSerMetAsnTyrrAlaAla 94
 Db 2055 GAGTC-AGGAGCAATTGTAAAGATCTMCC-----CTAAAGCT 2098

Qy 95 HisSerLysAspLysLysProGlnArg-----AspSerGlnAlaGln 109
 Db 2099 CC-AGCAAGGCCCCGGCCACCCGAAAGCCCACACCCGGAAAGAGGAGCTGTOAG 2157

Qy 110 LysSerProValLysSerThrHisArgIleGlnHisAsnIleAspTyrLeuLys 129
 Db 2158 AAGTCCTGGCACAGCAGGGCACCAAAACCGTTGGAACCAAACAAACCCAAA 2217

Qy 130 HisLeuSerLysValLysLysProSerAspPheGluGlySerGlyTyrThrAspIeu 149
 Db 2218 -----AAACCTGTCAAAGGCCCTTGCCCGGGCAGGTTAACGGCCAGGCTG 2262

Qy 150 GlnGluArgGlyAspAsnAspIleSerProHeSerGlyAspGlyinProHeSerAsp 169
 Db 2263 CAGGGGAAAGGGCAGGGCTTCTTCCTATGGCTCCCGAGACATTCAAAGAC 2322

Qy 170 IlePro-----GlyLysGlyGlu----- 175
 Db 2323 AAGGCCAAGGTGAAGGAAAGACGCCCGGGCCAGCAAGCAACGCA 2382

Qy 176 AlaThrIleProAspLeuGluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGlu 195

RESULT 10
 PCT-US94-04496-27
 ; Sequence 27, Application PC/TUUS9404496
 ; GENERAL INFORMATION:
 ; APPLICANT: Croce, Carlo
 ; TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
 ; TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
 ; TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1
 ; NUMBER OF SEQUENCES: 86

1 CORRESPONDENCE ADDRESS:
 1 ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewitz &
 1 ADDRESS: Norris
 1 STREET: One Liberty Place, 46th Floor
 1 CITY: Philadelphia
 1 STATE: Pennsylvania
 1 ZIP: 19103
 1 COMPUTER READABLE FORM:
 1 MEDIUM TYPE: Floppy disk
 1 COMPUTER: IBM PC compatible
 1 OPERATING SYSTEM: PC-DOS/MS-DOS
 1 SOFTWARE: PatentIn Release #1.0, Version #1.1.25
 1 CURRENT APPLICATION DATA:
 1 APPLICATION NUMBER: PCT/US94/04496
 1 FILING DATE:
 1 CLASSIFICATION:
 1 ATTORNEY/AGENT INFORMATION:
 1 NAME: DeLuca, Esg., Mark
 1 REGISTRATION NUMBER: 33,229
 1 REFERENCE DOCKET NUMBER: Tju-1242
 1 TELEPHONE: (215) 568-3100
 1 TELEFAX: (215) 568-3439
 1 INFORMATION FOR SEQ ID NO: 27:
 1 SEQUENCE CHARACTERISTICS:
 1 LENGTH: 9370 base pairs
 1 TYPE: nucleic acid
 1 STRANDBNESS: double
 1 TOPOLOGY: linear
 1 MOLECULE TYPE: DNA (genomic)
 1 FEATURE:
 1 NAME/KEY: CDS
 1 LOCATION: 469 .. 4032
 1 PCT-US94-04496-27

1 Alignment Scores:
 1 Pred. No.: 0.00499 Length: 9370
 1 Score: 137.00 Matches: 100
 1 Percent Similarity: 34.70% Conservative: 61
 1 Best Local Similarity: 21.55% Mismatches: 192
 1 Query Match: 6.01% Indels: 113
 1 DB: 5 Gaps: 17

1 US-09-700-696C-2 (1-430) x PCT-US94-04496-27 (1-9370)

1 Qy 37 AlaIleSerLysLeuHisAspGlnGluGluturyGlyAlaAlaLeuIleArgAsnAsnMet 56
 1 Db 1938 GCGATGCGACAACGTGGCTGACCAAAAGTGAAGCCAGCTGGCCACCAAGGGCCCCAG 1997
 1 Qy 57 GluHistLeMetGlyProValThrAlaIleLysLeuLeuGlyLysGluAsnLysGluAsn 76
 1 Db 1998 GAGCAC---AGGCCAAGCCCACGGGGCACCAAGAGTAAGGGCAGGTGGCAC 2054
 1 Qy 77 ThrProArgAsnValLeuAsn-----IleIleProAlaSerMetAsnTyraLysAla 94
 1 Db 2055 GAGTC-AGGCCRITCTGATCAAAGATCTAACAGCT 2098
 1 HisSerLysAspLysLysLysSerThrHisArgLysGlnHisAsnIleAspTyrLeuLys 129
 1 Db 2158 AAGTCCTCGGCACAGCGGGAGGCCCAAGCCAAGCCAAACGCCAA 2217
 1 Qy 130 HisLeuSerLysValLysLysLysLysSerAspPheGluGlySerGlyTyrThrAspLeu 149
 1 Db 2218 -----AAGCTGTCAGGCCCCACCGAACGCTGCCCCACGGTTAACGCCAGCTG 2262
 1 Qy 150 GluGluArgGlyAspAsnAspLysSerProAspPheGluGlySerGlyTyrThrAspLeu 169
 1 Db 2263 CAGGGGAAAGGGAGCCAGGGCTTCCTATGGCTCCGAGAACGACTTCCAAAAGAC 2322

1 170 IlePro-----GlyLysGlyGlu----- 175
 1 Qy 2323 AAGGCCAAGGTGAGGAGCAAGGGGCCGCGGCCAGCAACCCAAACCCAA 2382
 1 Db 176 AlaThrGlyProAspLeuGluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGlu 195
 1 Db 2383 GCAGTGCCCCCTCCAGTGAGAAGAGAACAGAGCTCCCTGCCCTCTAAG 2442
 1 Qy 196 AlaGluSer-----ThrHisLeuAspPheGlyProGlyTyr----- 208
 1 Db 2443 GCTCTCTAGGCCAGAACCCGGAAGGACAATGGAGACAGGCCCTGAGCATT 2502
 1 Qy 209 -----AspGluIleProGluArgGluGluAsnGlyGlyAsnThr 221
 1 Db 2503 GCTGTGTTCCCTGACTGAGGCCAGGCCACAGTCGAGCGCAGGGACT 2562
 1 Qy 222 IleGlyThrArgAspGluIleThrAlaLysGluAlaAspAlaValAspIle 241
 1 Db 2563 AGTGGCTGCGCCAAAGCCGTTGGTGGTCCAGGGAGCAGCCGAAAGACAGACTCCCATG 2622
 1 Qy 242 GlySerAsnAspIleMetGlySerIleLeuProGlyArgGluGlyAsn 261
 1 Db 2623 CCTTGAGAGAACCCAACTGCTCTACCGCTAGGGACTCTCCCAACAAAGCTG 2682
 1 Qy 266 ArgVal-----AspAlaGlySerGlnAsnAla 270
 1 Db 2683 ATGGGAGATACTCCATGACCTGCTCTCGGATACCCGCTCGCTCTCGGCTCTCGGAC 2742
 1 Qy 271 HisGlyGlyLysValGluPheHistYPTProProAlaProSerLysGlu 290
 1 Db 2743 CGCCAGAGAAACGAGATAAAACAGCCTGGCAGGGAAAGHAGCACAGCTCTGAGAG 2802
 1 Qy 291 GlySerSerAspAlaIleGluSerIleAsnIleGlyLysGly 310
 1 Db 2803 AGGAGCTCAGACAGCTCA-----AGCAAGTTGGCCAAAAGCAAAGGT 2847
 1 Qy 311 SerThrArgLysGlyValAspHisSerAsnArgGlnAlaThrLeuAsnGluLysGln 330
 1 Db 2848 GAGGAGAAAGAACACTGTGTAT----- 2880
 1 Qy 331 ArgPheProSerLysGlyLysserGlyLeuProIleProSerArgGlyLeuAspAsn 350
 1 Db 2881 AGA-----CTGGAGAG 2892
 1 Qy 351 GluIleLysAsnIleLysLeuAspSerPhenylAspSerAsnArgGlnAlaIleIleThr 369
 1 Db 2893 GAAATCAAATCAGCATCTCATCTCATCTCATCTCATCTCATCTAAACAAAG 2952
 1 Qy 370 -----HisGlyArgLysStyHistYtValProHisArgGlnAsn 382
 1 Db 2953 CCCTCAGGCCCTCTACAGTCCTAACAGGAAATGTCCTCCCGCCACCGTGNCC 3012
 1 Qy 383 AsnSerThrArgAsnLysGlyNetProGlyLysLysLysSer----- 396
 1 Db 3013 TCTCTCCCAAGGCCCTCCAAAAGTGGCAGGCAAGCTGCACTTAAGGGCTAACGCCAGCACC 3072
 1 Qy 397 TrpGlyIleGlnPro-----HisSerAsnArgArgHistSerSerGlu----- 409
 1 Db 3073 TCTGCGCAGGACCTCCAAAAGTGGCAGGCAACCAAGAACGACTCTCC 3132
 1 Qy 410 ArgArgArgAspSerSerLysLysSerSerLysSerSerGlu----- 426
 1 Db 3133 ATTCCCAAGCAGGAGGAGGAACTCCAAAGCTCCGAGCACAGGGTT 3192
 1 Qy 427 SerAspGlyAsp 430
 1 ; Sequence 25, Application US/08320559
 1 ; Patent No. 5633135

1 RESULT 11
 1 US-08-320-559-25

2644 CCTTGAGACCAAGGTGCTCACCGCTCAGGGAGACTCTCCCCACAAAGCTTG 2703
 QY 262 ArgVal-----AspAlaGlySerGlnAsnAla 270
 Db 2704 ATGGTGAAGATCACCTAGACCTGCTCTCGGATAACCCAGCCTCCGGGAGGGAGC 2763
 QY 271 HisGlnGlyLysValGlutheHistYProProProLysAla 290
 Db 2764 CGCCAGGGAAAGGAAAGATAAACGCCGCCAGGGAAAGAGCAAGCTCTGAGAG 2823
 QY 291 GlySerSerAspAlaAlaGluSerThrAsnTyrAsnGluLeuProLysGly 310
 Db 2824 AGGAGCTGAGCTCA-----AGCAACTGGCCAAlAAGAGAAACGGT 2868
 QY 311 SerThrArgLysGlyValAspHisSerAsnArgAsnGlnAlaThrLeuAsnGluLysGln 330
 Db 2869 GAGGCAAAAGAGAGACTGAT-----AACAGAAAATC 2901
 QY 331 ArgPheProSerLysGlyLysSerGlnGlyLeuProLeuProSerArgGlyLeuAspAsn 350
 Db 2902 AGA-----CTGGAGAG 2913
 Alignment Scores:
 Prod. No.: 0.00501 Length: 9391
 Score: 137.00 Matches: 100
 Percent Similarity: 34.70% Conservative: 61
 Best Local Similarity: 21.55% Mismatches: 192
 Query Match: 6.01% Indels: 113
 DB: 5 Gaps: 17

US-09-700-696C-2 (1-430) x PCT-US94-04496-25 (1-9391)
 Qy 37 AlanineSerLysLeuHisAspGlnGluLutYrGlyAlaAlaLeuIleArgAsnAsnMet 56
 Db 1959 GCGCTGGACAATCTGGTGAACGACGCCACGCCAGCTGCACGCCAG 2018
 Qy 57 GluHistLeMetGlyProValThrAlaLysLeuLysGlyLysGluIuAsnLysGluAsn 76
 Db 2019 GACAC-----AGAGCCCACGGGAGACCCAGAGAGTAAGGAGCTGACGTGCCAG 2075
 Qy 77 ThrProArgAsnValLeuAsn-----IleIleProAlaSerMetAsnTyralAlaSala 94
 Db 2076 GACTC-ACGAGCATTCTGAATCCAAGAATCTCTCC-----CTAAAGCT 2119
 Qy 95 HisSerLysAspLysLysProGlnArg-----AspSerGlnAlaGln 109
 Db 2120 CC-AGCAAAGGCCCGCCGGCCAACCGGAAGAGGAGCTGTGAG 2178
 Qy 110 LysSerProLysSerLysSerThrHisArgIleAspTyrlLeuIys 129
 Db 2179 AGTCTCGGACAGCGAGGCCAACAAACGCCAAACGCCAA 2238
 Qy 130 HisLeuUserLysSilleProSerAspHeGluGlySerGlyTyrlThrasIle 149
 Db 2239 -----AAACCTCTCAAGGCCCTGCGGGAGGTCAAGGACCAACGCCAA 2283
 Qy 150 GluGluLargGlyAspAsnAspLysProHeSerSerLysProHeLysAsp 169
 Db 2284 CAGGGAAAAGGGAGCCAGGCTTCCTPATGGCTCCAGACACTCCAAAGAC 2343
 RESULT 13
 PCT-US94-04496-25
 Sequence 25, Application PC/TUS9404496
 GENERAL INFORMATION:
 APPLICANT: Croce, Carlo
 APPLICANT: Canaan, Eli
 TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
 TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
 NUMBER OF SEQUENCES: 86
 ADDRESS: Woodcock, Washburn, Kurtz, Macklewitz &
 ADDRESSEE: Morris
 STREET: One Liberty Place, 46th floor
 CITY: Philadelphia
 STATE: Pennsylvania
 COUNTRY: USA
 ZIP: 19103
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/04496
 FILING DATE:
 CLASSIFICATION:

2524 GCTCTTGTTCCTGACTGAGAGCCACACAGTGGCAGCAGCACT 2583

QY 176 -----AlaThrGlyProAspLeuGluGlyLysAspIleGlnThrGlyPheAlaGly 192
 Db 2201 ACTGCAAGCGTTAACGGTATTGCGAAAGCTGGAAAGGA---AACTTAGGGCATCAAAT 2257
 QY 193 ProSerGluAlaGluSerThrHisLeuAspThrLysLysProGly----- 207
 Db 2258 AGTCGACCTTCAGTCCACC---GTGAGACCAATAAGCCAGGTGATGATACTGTGAAAC 2314
 QY 208 -----TyrAsnGluIle 211
 Db 2315 AGTCGATCTATACTCTAGTGAGTGCGCAAAACCATGGTAACCCCTATATGGTTG 2374
 QY 212 ProGluLargGluGluAsnGlyGlyAsn-----Thr 221
 Db 2375 AGCATTGAAAGACAATAGTGTAGCATGGCTGACCTGGATCAATGGGATCCCTGAT 2434
 QY 222 IleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGlu 241
 Db 2435 TCAAATAGTAAAGGTGACAGCGAAAACGGCAAGATAATGATAATGCCAAGGCTACTAA 2494
 QY 242 GlySerAsnAspIleMetGlySerThrAsnPhyLysGluLeuProGlyArgGluGly 261
 Db 2495 GATAGTACTAAATGGTCAGATGTGTCAGCGACTGCA 2539
 QY 262 ArgValAspAlaGlySerGlnAsnAlaLysGlnGlyLysValGluPheHistyrProPro 281
 Db 2540 ACTACTATGCCACTGTGAGGAAATTAAAGGTTCTGAGGATGGATAAACT 2599
 QY 282 AlaProSerLysGluLysGluLysSer-----AspAlaAlaGluUser 298
 Db 2600 GTAGGAATGAAATGAGGAGGGGGAGATACTCTGAATAAAGGTGACCGACTGTA 2659
 QY 299 ThrAspThrAsnGluIleProGlySerGlyLysGlyLysValGluPheHistyrSerThr 315
 Db 2660 GTTGGTGAGGATAATTGGTGAACAGCCCTGGTGTCTAGACTAAATGATGATCAAA 2719
 QY 316 ValAspHisSerAsnArgAsnGlnAlaThrLeuAsnGluLysGlnArg-----PhePro 333
 Db 2720 AATGACAGGAAAAGAACGGGSCCTAACCTGACAGTAACAGATGCACT 2779
 QY 334 SerLysGlySerGlnGlyLeuProSerArgGly-----LeuAspAsnGlu 351
 Db 2780 GGCTTAAGTAAACCGAAAGTTAGAATCAAAAGAAAGTGGAGATAGAACTTAATGAT 2839
 QY 352 IleLysAsnGluMetAspSerProAspGlyProSerHisGluAsnIleThrHisGly 371
 Db 2840 ACAACTAACAGTTAGAAATAAAAATGGAGAAAAGAAACGGAATCATGATG 2899
 QY 372 ArgLysGlyHistyrValProHisArgGlnAsnAsnSerThrArg----- 386
 Db 2900 TTAAAAGTAAATGAGCATGCCAATGAGAACAAACTCTGACAAACTGAGATGCGAA 2959
 QY 387 -----AsnLysGlyMetProGlyLysGlySerTrpGlyArgGlnProHisSer 403
 Db 2960 GGACATGACAGGATAGCATCAAATGATAAACGGAAGCATATG 3013
 QY 404 AsnArg---ArgPheSerSerArgArgAspAspSerSerGluUserSerAspArgGly 422
 Db 3014 ATAAGGATATTGTTACGAAAATAACAAATAGTCACATTAAATGATAATAATTG 3073
 QY 423 SerSerSerGluSerAsp 428
 Db 3074 AGTAACTGAAATAATTGAT 3091
 QY 15 HisAspGlnGluGluTyrGlyAlaAlaLeuIleArgAsnAsnThrProArgAsn 80
 Db 1859 GCATATAATTGAGTTGTTGTTGTTGCGTTGAGGCTTAAATAATCAGGAGTT 1918
 QY 81 ValLeuAsnIleProAspSerMetAsnTyraLysAlaHisSerLysAspLysLys 100
 Db 1802 ---GACTTAGATGAAATTAAACGAGTTGGCTTGTGAGATGAAATGAAACGTTGTTG 1858
 QY 62 ProValThrAlaIleLysLeuIleGly---GluGluAsnIleGluAsnThrProArgAsn 80
 Db 1859 GCATATAATTGAGTTGTTGTTGTTGCGTTGAGGCTTAAATAATCAGGAGTT 1918
 QY 81 ValLeuAsnIleProAspSerMetAsnTyraLysAlaHisSerLysAspLysLys 100
 Db 1802 ---GACTTAGATGAAATTAAACGAGTTGGCTTGTGAGATGAAATGAAACGTTGTTG 1858
 QY 101 LysProGlnLargAspSerSerGlnAlaGlnLysSerProValLysSerThrHisArg 120

RESULT 15
 US-09-487-826B-1
 Sequence 1, Application US/08487826B
 Patent No. 593827
 GENERAL INFORMATION:
 APPLICANT: Sim, Kim L.
 APPLICANT: Chitnis, Chetan
 APPLICANT: Miller, Louis H.

Db	1976 CAGCTGTAGATGAAAGGGAGAAGGTTCCA-----GGAGATTCTACGGAT----	2026	Qy	423 SerSerSerGluSerAsp	428
Qy	121 IleGlnHisAsnIleAspTyrLeuLysHisLeuSerLysVal---LysLysIleProSer	139	Db	3074 AGTATGGAAAATTAGAT	3091
Db	2027 -----GAAATGTTAACAGGGCAAGAGTAGTTCTACACAGGTAAAGCTGTACGGGG	2080		Search completed: November 30, 2003, 02:11:35	
Qy	140 AspPheGluGlySerGlyTyrrThrasPleGln-----GluArgGlyAspAsnAsp	156		Job time : 115 secs	
Db	2081 GATGTCATAATGGAAATCAGACACTGGAGAAAGCGATGTACCGGAAGTGTATTGCC	2140			
Qy	157 IleSerProheSerLysAspGlyGlnInproheLysAspIleProGlyLysGlyGlu---	175			
Db	2141 GAAAGTGTAACTGCTRAAAATGTTGATTCGAGAAATCTGTAAGTAAGAAAGTGACGAC	2200			
Qy	176 -----AlaThrGlyProAspIleGluGlyLysAspIleGlnThrGlyPheAlaGly	192			
Db	2201 ACTGAAAGGTTACGGTATGGTGTACGTTGCTGCAAGGCGAAAGGAA--AACTTACGCGATCAAAT	2257			
Qy	193 ProSerGluAlaGluSerThrHisLeuAspThrLysPheGly-----	207			
Db	2258 AGTCGACCTCTGACTCCACC--GTTGAGCAAAATGCCAACGGTGTACACTGTGAAAC	2314			
Qy	208 -----TyrAsnIle	211			
Db	2315 AGTCGATCTATAACCTGTTAGTGACTGTGGTAAAACCCATTGGTAACCCCTATAATGGTTG	2374			
Qy	2112 ProGluArgGluAsnGlyGlyAsn-----	221			
Db	2375 AGGCATTCCAAAGCAATAATGATAGCGATGGGACTCGGCAATCATGGGAATCTGTGT	2434			
Qy	2222 IleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGlu	241			
Db	2435 TCAAAATGAAAGGTGAGACGGAAAGGGCAAGATAATGATACTGGAAAGGCTACTATA	2494			
Qy	2442 GlySerAsnAspIleMetGlySerThrAsnPhenylAsnGlyAsn	261			
Db	2495 GATACTGAAATAGTTCAAGATGGTACCGAC-----TCCTCTACGGGTGAT	2539			
Qy	2162 ArgValAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluHistidylProPro	281			
Db	2540 ACTACTGAGCAGTGTATGGAAATTATAAAGGTGTCTGGGATGGGATAAACCT	2599			
Qy	2832 AlaProSerLysGluLysArgLysGluGlySerSer-----AspAlaAlaGluSer	298			
Db	2600 GTAGGAAGTAAAGATGGAGACGGGGAAAGATAACITGCUAAATAAGGATCAGGCACTGNA	2659			
Qy	2999 ThrasnTyrAsnGluIleProLysAsnGlyLysLysThr-----ArgLysGly	315			
Db	2720 AATGACACGGAAAAGAACCGGGCTCTACCCCTGACGTAAGAACGAGGATGCAACT	2779			
Qy	334 SerLysGlyLysSerGlnGlyLeuProIleProSerArgGly-----LeuAspAsnGlu	351			
Db	2780 GCGCTTAACTAACCGAAAGTTGAGATACAGAAAAGTGAATACAGAAAAGTGAGATGAACTACTAATGAT	2839			
Qy	352 IleLysAsnGluIleAspSerPheAsnGlyProSerHisGluAsnIleLeuThrHisGly	371			
Db	2840 ACAACTAACTGTTAGAAATAAAATGGGAAAAGAAAAGGTTACAAAGCATA	2899			
Qy	372 ArgLysTyrHistidylValProHisArgLysAsnSerThrArg-----	386			
Db	2900 TTAAAAGTATGATACCGGAATGAAAGACCAATTCTGATCAACTACAGATGCGAGAA	2959			
Qy	387 -----AsnLysGlyMetProGlyLysGlySerTrpGlyArgGlnProHisser	403			
Db	2960 GGACATGAGCAGGGATAGCTCAAAATGATAAAGCAGAA-----AGGAAAGCCATATG	3013			
Qy	404 AsnArg--ArgPheSerIleArgArgAspSerSerGluSerSerIspSerIly	422			
Db	3014 AAAAAGATTAATTTACGAAAAATAATACAAATAATAGTCACCATTAATAGTATAATG	3073			

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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 30, 2003, 00:14:26 ; Search time 423 Seconds (without alignments)

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Title: US-09-700-696C-2

Perfect score: 2279

Sequence: 1 VNKVEISNKRENTHGLRMS.....RRDDSESSSDGSSESSESGD 430

Searched: 3349.212 Million cell updates/sec

Total number of hits satisfying chosen parameters: 4380138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q //cgn2.1/uspto.spool//us09700896/runat_26112003_152634_14705/app_query.fasta_1.583
-DB=publi.shed.APPLICATIONS.NA -QMT=rastap -SURFTX=blobsum62
-LOPCL=0 -LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIXX=blobsum62
-TRANS=human40_cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=dto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US0970096 @CGN 1.221 @runat_26112003_152634_14705
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-LONGLOG -TIMEOUT=30 -WARN TIMEOUT=30 -THREADS=1 -XGAPPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPEXT=0.5 -DELEXT=7
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Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1 US-10-311-840-2

; Sequence 2, Application US-10311840

; Publication No. US20030175805A1

; GENERAL INFORMATION:

; APPLICANT: KUROKAWA, Tomofumi

; APPLICANT: YAMADA, Takao

; APPLICANT: MORIMOTO, Shigeto

; TITLE OF INVENTION: No. US20030175805A1el Protein and its DNA

; FILE REFERENCE: 2739USOP

; CURRENT APPLICATION NUMBER: US-10/311,840

; CURRENT FILING DATE: 2002-12-18

; PRIOR APPLICATION NUMBER: PCT/JP01/05263

; PRIOR FILING DATE: 2001-06-20

; PRIOR APPLICATION NUMBER: JP 2000-191088

; PRIOR FILING DATE: 2000-06-21

; NUMBER OF SEQ ID NOS: 10

; SEQ ID NO: 2

; LENGTH: 1575

; TYPE: DNA

; ORGANISM: Human

Alignment Scores:

Result No.	Query Length	Match Length	DB ID	Description
1	2276	99.9	1575	US-10-311-840-2

SUMMARIES

Result No.	Query Length	Match Length	DB ID	Description
1	2276	99.9	1575	US-10-311-840-2

Length: 1575
Pred. No.: 2.22e-213
Alignment Scores: 1.0

Page 1575

Sequence 33, Application US/09794422
 ; Publication No. US20030166239A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brown, Thomas A.
 ; APPLICANT: De Wet, Jeffrey R.
 ; APPLICANT: Gowen, Lori C.
 ; APPLICANT: Hames, Lynn M.
 ; TITLE OF INVENTION: Mammalian Osteoregulins
 ; FILE REFERENCE: PC10445
 ; CURRENT APPLICATION NUMBER: US/09/794,422
 ; CURRENT FILING DATE: 2001-02-27
 ; PRIOR APPLICATION NUMBER: 60/185,617
 ; PRIOR FILING DATE: 2000-02-29
 ; PRIOR APPLICATION NUMBER: 60/234,500
 ; PRIOR FILING DATE: 2000-08-22
 ; NUMBER OF SEQ ID NOS: 46
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO: 33
 ; LENGTH: 1876
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-794-422-33
 ;
 Alignment Scores:
 Pred. No.: 2.78e-213 Length: 1876
 Score: 2276.00 Matches: 429
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 99.77% Mismatches: 0
 Query Match: 99.87% Indels: 0
 DB: 12 Gaps: 0
 US-09-700-696C-2 (1-430) x US-09-794-422-33 (1-1876)
 Qy 1 ValAsnLysGluTyrSerAlaSerAlaLysGluAsnThrHisAsnGlyLeuArgMetSer 20
 Db 238 CTGAATAAAGATAATACTATCGATACAAAGATACTACAATGCCCTGAGGTGTC 297
 Qy 21 IleTerProllysSerThrGlyAsnLysGlyPheGluaspGlyAspSpalaiIleSerLys 40
 Db 298 ATTATCTCTAGTCAGTCAGCTGGAAATTAAGGTTTGAGATGGATGGATGCTAC 357
 Qy 41 LeuHisAspGlnGluGluIutrglyAlaAlaLeuIleArgAsnAsnMetGlnHisIleMet 60
 Db 358 CTCATGACCAGAGAAATATGGGAGCTCATAGAAAATAACTGCAACATATAATG 417
 Qy 61 GLYProvalThrAlaIleLysLeuIleGlyGluGluAsnLysGluAsnThrProArgAsn 80
 Db 418 GGCCAGGACTGCGATTAACTCTGGGAAAGAAACAGAACACTGAGATGGATGG 477
 Qy 81 ValLeuAsnIleIleProAlaSerMetAsnTyrralaLysAlaHiSerLysAspLysLys 100
 Db 478 GTCCTAACATATCCAGAAGTAAATTATGCCAGAATTTATGCCAGATGAACTGAA 537
 Qy 101 LysProGlnArgAspSerGlnAlaGlnLysSerProValLysSerThrHisArg 120
 Db 538 AAGCCCTAAAGAGATTCCTAACGCCAACCTTCAGCTCGTAAAGTGTAAAGGCA 597
 Qy 121 IleGlnLisAsnIleAspTyrralaLysLeuSerLysValLysIleProSerAsp 140
 Db 598 ATTCAACACATTCGTTAAACATCTCTGAACTTCAGGAACTTCAGGAACT 657
 Qy 141 PheGluGlySerGlyTerThrAspIleGluGlyGluArgLysAspAsnAspIleSerProPhe 160
 Db 658 TTGAAGGGCGGGTATAAGATCTCAAGGAGGGACATATTCAGAGGGGACAAT 717
 Qy 161 SerGlyAspGlyGlnProphelyAspIleProGlyLysGlyGluIutrglyProAsp 180
 Db 718 AcneGACGGCAACCTTAAAGGACATTCCTGAAAGAGAMCTACTGGTCGTGAC 777
 Qy 181 LeuGluGlyLysAspIleGluGlyTerThrGlyPheAlaGluSerThrHis 200
 Db 778 CTAGAACCCAAGATATTCAAACGGCTTGCAGGCCAAGTAGCTGAGACTCAT 837
 RESULT 3
 US-09-794-422-33

QY 201 LeuAspThrLysProGlyTyrAsnGluIleProGluArgGluAsnGlyGlyAsn 220
 Db 838 CTTACACAAAAAGCCAGTTATAATGGATCCAGAGAAATGGGAATT 897

QY 221 ThrIleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValSerLeuVal 240
 Db 898 ACCATTGGAACTTGGATGAAACTCGCAAGAGGCCAGATGCTGTGATTCAGCCTTGCA 957

QY 241 GluGlySerAsnAspIleNetGlySerThrAsnHeLysIleLeuProGlyArgGluGly 260
 Db 958 GAGGCAGGAACGATATCATGGTAGTACCAATTAAAGGTCCTCGAGAAGAGCA 1017

QY 261 AsnArgValAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHisTyrPro 280
 Db 1018 AACAGAGTGGATGTGGCCAAAATGGTCACCAAGGGAAAGGTGAGTTTACCT 1077

QY 281 ProAlaProSerLysGluIysArgLysGluGlySerSerAspAlaAlaGluUserThrAsn 300
 Db 1078 CCTGCACCTCAAAGAGAAAAGAGGCCAGTGTGATGCACTGAAAGTACCAAC 1137

QY 301 TyrAsnGluIleProLysAsnGlyLysGlySerThrArgLysGlyLysValAspHisSerAsn 320
 Db 1138 TATATGAAATTCTAAATGGCAAGGCGTACCAAGAACGCAATTCTAAAT 1197

QY 321 ArgAsnGlnAlaThrLeuIleGlyLysGluIleProSerLysGlyLysSerGlnArgPhe 340
 Db 1198 AGAACCAAGCAACCTTAATGAAAACAAAGTTCTCTAGTAAAGTCAGGCG 1257

QY 341 LeuProIleProSerArgIleLeuAspSerGluMetAspSerPheAsn 360
 Db 1258 CTGCCATTCCTCTCGTGTCTGATATGAAATGAAATGCTTAAAT 1317

QY 361 GlyProSerThrGluAsnIleThrHisGlyArgLysTyrHistYvalProHisArg 380
 Db 1318 GGCCCGAGCATGAAATAAACATGGCGAAATAATCATTTGACCCACAGA 1377

QY 381 GlnAsnAsnSerThrArgAsnLysGlySerTrpGlyArgLysGly 400
 Db 1378 CAAAATAATTCTACAGGATAACGGATGCCAACAGGCAAGCTCTGGGTAGACA 1437

QY 401 ProIleSerAsnArgArgPheserSerArgAspSerSerGluUserSerAsp 420
 Db 1438 CCCCATTCACAGGAGTTAGTTCCCGTAGAGGGTACAGTAGTCATCIGCA 1497

QY 421 SerGlySerSerGluUserAspGlyAsp 430
 Db 1498 AGGGCAGITCAAGTGAGCGATGGTCAAC 1527

RESULT 4
 US-09-794-422-45
 ; Sequence 45, Application US/09794422
 ; GENERAL INFORMATION:
 ; Publication No. US200301662391
 ; APPLICANT: Brown, Thomas A.
 ; De Wet, Jeffrey R.
 ; APPLICANT: Gowen, Lori C.
 ; APPLICANT: Hames, Lynn M.
 ; TITLE OF INVENTION: Mammalian Osteoregulins
 ; FILE REFERENCE: PC10445
 ; CURRENT APPLICATION NUMBER: US/09794422
 ; CURRENT FILING DATE: 2001-02-27
 ; PRIORITY NUMBER: 60/185,617
 ; PRIORITY FILING DATE: 2000-02-19
 ; PRIORITY NUMBER: 60/234,500
 ; PRIORITY FILING DATE: 2000-09-22
 ; NUMBER OF SEQ ID NOS: 46
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 45
 ; LENGTH: 1969
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-794-422-45

QY 241 GluGlySerAsnAspIleMercylySerThrAsnPhelysGluLeuProGlyArgGluGly 260
 Db 1051 GAGGCAGCAACGATATCATGGGTAGTAACTTAAAGGACTCCTGGAGAGAGGA 1110

QY 221 ThrIleGlyThrArgAspGluThraLysGluAlaAspAlaValAspValSerLeuVal 240
 Db 991 ACCATGGAACTAGGATGAAACTGCCAACGGCAATGCTGTTAGTCAGCCCTGA 1050

QY 241 GluGlySerAsnAspIleMercylySerThrAsnPhelysGluLeuProGlyArgGluGly 280
 Db 1111 AACAGACTGGATGCTGCCAGCCAATGCTCACCAAGGGAGGGTCAGTTGTCATTCACCT 1170

QY 281 ProAlaProSerLysGluIysArgLysGlySerSerAspAlaAlaGluSerThrAsn 300
 Db 1171 CCTGCACCTCAAAGGAAAGAAGAAAGGCAATGAGTGTGACCTGAAAGTACAAAC 1230

QY 301 TyrAsnGluIleProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsn 320
 Db 1231 TATAAGAAATTCTAAAGGAAAGAAGAAAGGCAATGAGTGTGACCTGAAAGTACAAAC 1290

321	ArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlyLys 340	Qy	
1231	AGAACCAAGCAACCTTAATGAAAACAAGGTTCCPAGTAACGGCAAAAGTAGGGC 1350	Db	
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; Sequence 5 , Application US/09794422			
; Publication No. US20030166239A1			
; GENERAL INFORMATION:			
; APPLICANT: Brown, Thomas A.			
; DE WET, Jeffrey R.			
; APPLICANT: Gowen, Lori C.			
; APPLICANT: Hames, Lynn M.			
; TITLE OF INVENTION: Mammalian Osteoregulins			
; FILE REFERENCE: PCL0445			
; CURRENT APPLICATION NUMBER: US/09/794,422			
; CURRENT FILING DATE: 2001-07-27			
; PRIOR APPLICATION NUMBER: 60/185,617			
; PRIOR FILING DATE: 2000-02-29			
; PRIOR APPLICATION NUMBER: 60/234,500			
; PRIOR FILING DATE: 2000-09-22			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 5			
; LENGTH: 2019			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; US -09-794-422-5			
Alignment Scores:			
Pred. No.:	3.06e-213	Length:	2019
Score:	2276.00	Matches:	429
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.77%	Mismatches:	0
Query Match:	99.87%	Indels:	0
DB:	12	Gaps:	0
US -09-700-696C-2 (1-430) x US -09-794-422-5 (1-2019)			
Qy	1 ValAsnLysGluLysSerIleSerAsnLysGluAsnThrHisAsnGlyLysLeuArgMetSer 20	Qy	
Db	381 CTGAAATAAGATAATAGTATCAAAAGGAAATACTCACATGGCTGAGATGTCA 440	Db	
Qy	21 IleTyrProLysSerThrGlyAsnLysGlyLysGlySerGluLysGlyAspAspAlaIleSerLys 40	Qy	
Db	441 ATTATTCCTAATCTGGAAATAAGGTTAGGATGGCTGAGATGTCA 500	Db	
Qy	41 LeuHisAspGlyGluGluGlyLysGluAsnLysGluAsnThrProArgAsn 60	Qy	
Db	501 CTACATGACCAAGAAAGATACTGGCAAGCTCTCATGAAATAACATCAATAATG 560	Qy	
Qy	561 GGGCCATGACTCGATAACTCTGGGGAGAAACAAAGGAAACACCTTGAAT 620	Qy	
Qy	81 ValLeuAsnIleLeuProAlaSerMetAsnTyrAlaLysSerLysAspLysLys 100	Qy	
Db	621 GTTCTAAACATATCCCGCAACTATGGATTATCTAACGCAACTCTGAGGATAAAAG 680	Db	
Qy	101 LysProGlnArgLysSerGlnAlaGlnLysSerProValLysSerThrIleArg 120	Qy	
Db	681 AACGCCTCAAAAGGATTCGGCAACCTTAAAGGACCCATCTGT 740	Db	
Qy	121 IleGlnHisAsnIleAspTyrIleLeuLysSerLysSerThrIleProSerAsp 140	Qy	
Db	741 ATTCAACACAACTTCAAAAGTCAAATGCTTCAAGGAGGACTACTGGTCTGAC 800	Db	
Qy	141 PheGluGlySerGlyTyrThrAspLeuGlnGluArgGlyAspAlaSerProPhe 160	Qy	
Db	801 TTGAAAGCAGGGCCACCTTAAAGGACATTCCTGTAAGGAGGACTACTGGTCTGAC 860	Db	
Qy	161 SerGlyAspGlyGlyLysProGlyLysGlyGluLysGluAlaGluSerThrHis 200	Qy	
Db	921 CTAGAACCCAAAGGATTCRAACGGCTTCAGGCTGACTGAGTCACTCAT 980	Db	
Qy	201 LeuGluGlyLysAspIleMetGluLysGlyPheAlaGlyProSerGluAlaGluSerThrHis 220	Qy	
Db	981 CTTGACACAAAAAGGCAAGGTTAAATAGATCCCAAGGTTAACTGAGTCACTCAT 1040	Db	
Qy	221 ThrIleGlyIleArgAspGluIleAlaLysGluLysGlyLysGly 240	Qy	
Db	1041 ACCATGGAAACTAGGGATGAAACTCTGCAAAAGGGAGATGCTGAGTCTGGCTGAG 1100	Db	
Qy	241 GluGlySerAsnAspIleMetGlySerThrAsnPhelysGluLeuProGlyIleArg 260	Qy	
Db	1101 GAGGGAGCAACGATATCATGGCTGAACTTAAAGGAGCTCCCTGGAAGGGAGGA 1160	Db	
Qy	261 AsnArgValAspAlaGlySerGlnAsnAlaLysGlnGlyLysValGluPheHistYrPro 280	Qy	
Db	1161 AACAGACTGATGCTGCGAGCCAAAGGCAACTACGCAAGGCAACTACCT 1220	Db	
Qy	281 ProAlaProSerLysGluLysBrgLysGluGlySerSerAspAlaAlaGluSerThrAsn 300	Qy	
Db	1221 CCTGCACCCCTCAAAGGAAAGAAAGAAAGGAGGAGTACTGATCAGCTGAAAGTAC 1280	Db	
Qy	301 TyrAspGluIleProLysAsnGlyLysGlySerIleSerGlyLysValAspHisSerAsn 320	Qy	
Db	1281 TATAATGAAATTCCTTAAAGTCGCAAAAGGCAACTACGCAAGGCAACTACCT 1340	Db	
Qy	321 ArgAsnGlnAlaThrLeuAsnGluLysGlySerGlnArgPheProSerLysGlyLysGly 340	Qy	
Db	1341 AGGAACCAAGGAAACCTTAATGAAACAAAGTTCAGGTTCTAGTAAGGGAAAATCATATGTCAGGCTGAG 1520	Db	
Qy	341 LeuProIleProSerArgGlyIleAspAsnGluLysSerGlySerGlnArgLys 360	Qy	
Db	1401 CTGCCATTCTCTCTGCTGCTGATAATGAAATCTGAACTCTTAAAT 1460	Db	
Qy	361 GlyProSerHisGluAsnIleIleThrHisGlyArgLysSthIleSerGlySerGlnArgPheProSerLysGlyLysGly 380	Qy	
Db	1461 GGCCCCAGTCATGAGGATAATATAACATGCGAAATAATCATATGTCACCCACAGGA 1580	Db	
Qy	381 GlnAsnAsnSerThrArgAsnLysGlyMetProGlyLysGlySerTyrGlyArgGln 400	Qy	
Db	1521 CAAATANITCTACGGGATAAGGGTGTAGGCTGAGCTGAGCTCATCTGAC 1640	Db	
Qy	401 ProHisSerAsnArgArgPheSerSerArgArgAspSerSerGluSerSerAsp 420	Qy	
Db	1581 CCCCATTCACAGGAGGTTAGTCCTCCGGTAAGGAGGATGACAGTGTGAC 430	Db	
Qy	421 SerglySerSerSerGluIleLeuLysLeuSerAspGlyYaspGlyYasp 430	Qy	

Db 1641 AGTGGCAGTCAACTGAGGCGATCTGTGAC 1670
 RESULT 6
 US-09-794-422-7
 ; Sequence 7 Application US/09794422
 ; Publication No. US20030166239A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brown, Thomas A.
 ; De Wet, Jeffrey R.
 ; APPLICANT: Gowen, Lori C.
 ; APPLICANT: Hames, Lynn M.
 ; TITLE OF INVENTION: Mammalian Osteoregulins
 ; FILE REFERENCE: PCT04/045
 ; CURRENT FILING DATE: 2001-02-27
 ; PRIOR APPLICATION NUMBER: 60/1185, 617
 ; PRIOR FILING DATE: 2000-02-29
 ; PRIOR APPLICATION NUMBER: 60/234, 500
 ; PRIOR FILING DATE: 2000-09-22
 ; NUMBER OF SEQ ID NOS: 46
 ; SOFTWARE: PatentIn ver. 2.0
 ; SEQ ID NO: 7
 ; LENGTH: 2112
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-794-422-7

Alignment Scores:
 Pred. No.: 3.25e-213 Length: 2112
 Score: 2276.00 Matches: 429
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 99.77%
 Query Match: 99.87%
 DB: 12
 DB: 12 Gaps: 0

US-09-700-696C-2 (1-430) × US-09-794-422-7 (1-2112)

Qy 1 ValAsnLysGlnThrSerLeuAsnLysGluAsnThrHi sAsnGlyLeuArgMetSer 20
 Db 474 CTGTAATAGAATATACTATGTAACAAAGATACTACATGGCTGAGGTGTCA 533
 Qy 21 IleTyrProLysSerThrGlyAsnLysGlyPheGluAspAlaIleSerLys 40
 Db 534 ATTATCTAACGTCAAACGGATAAANGGTTGAGATGATGCTATCGCAA 593
 Qy 41 LeuHisAspGlnGluGlyIleValAlaLeuIleArgAsnAsnMerGlnHistMet 60
 Db 594 CTCATGCCCCAGAAGATACTGCAGTCATCGAAATACTCGAACATAATG 653
 Qy 61 GlyProValThrAlaIleLysLeuLysGluGluAsnLysGluAsnThrProArgAsn 80
 Db 654 GGCGCAAGTGACTCGATTAACTCTGGGGAGAAAACAGAGAACACCTAGAA 713
 Qy 81 ValLeuAsnIleLeuProAlaSerMetAsnTyralAlaAlaIleSerLysAlaAlaIleSerLys 100
 Db 714 GTCCTAACATAATCCCGCAACTATAATTGCTAAAGCACACTGAACTAAAG 773
 Qy 101 LysProGlnArgAspSerGlnAlaGlnLysSerProValLeuSerLysSerThrHi sArg 120
 Db 774 AACCTCTAAAGATTCAGAAAGCTCCAAAGGCCAAAGTCCAGAAAGCACCCTCT 833
 Qy 121 IleGlnHisAsnIleAspTyrLeuLysIleLeuSerLysIleProSerAsp 140
 Db 834 ATCCAACACAACATGCTACTAAACATCCTCTCAAACTCAAAACTCAAA 893
 Qy 141 PheGluGlySerGlyTyrThrAspLeuGluArgGlyAspAsnAspSerProAsp 160
 Db 894 TTGAAGGGAGGCCTTAAACAGTCCTTAAGGAGAGGGACATGATATCTCTTC 953
 Qy 161 SerGlyAspGlySerProGlyLysGlyGluAlaThrGlyProAsp 180
 Db 954 AGTGGCAGTCAGTCAGTGAAGGAAAGTCTGGTCCCTGAC 1013

Qy 181 LeuGluGlyLysAspIleGlnThrGlyPheAlaGluGluAlaGluAspSerThrHis 200
 Db 1014 CTGAGCCAAAGATTTCAACAGCTTTCAGGCCAACTGAACTGAGGACTCAT 1073
 Qy 201 LeuAspThrIleLysProGlyTyrArgGlyLysGluAsnGlyGlyAsn 220
 Db 1074 CTTGACACAAAAAGCAGTTATATGAGATCCCAGAGAGAAAATGGTCAAAT 1133
 Qy 221 ThrIleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValSerLeuVal 240
 Db 1134 ACCATTGAACTAGGATGAAACTGCAAGGGGATGCTGTCATGAGCTGTGA 1193
 Qy 241 GluGlySerAsnAspIleMetGlySerThrAsnPhenylAspSerLeuProGlyArgGluGly 260
 Db 11394 GAGGCGAGCAACATACATGGTAGTACATTAAAGGCTCCCTGAAAGAGAGGA 1253
 Qy 261 AsnArgValAspAlaGlySerGlnAsnAlaLysGlnGlyLysValGluPheHistYrPro 280
 Db 1254 AACAGATGGGATGCTGCAGCCAAATGTCACCAAGGAGGTGAGTTCAATCCCT 1313
 Qy 281 ProAlaProSerLysGluIleGlySerLysArgLysGluGlySerSerAspAlaAlaGluSerThrAsn 300
 Db 1314 CCTGCACCTCTAAAGGAAAGAAAGAAAGAAAGCAGCCAAATGTCACGAGTGCAGTGCAGT 1373
 Qy 301 TYTAsnGluIleProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsn 320
 Db 1374 TATAATGAAATCTCTAAATGCAAGGCAAGGCTACCGAAAGGCTGATCATCTTAAT 1433
 Qy 321 ArgAsnGlnIleThrLeuAsnGlyLysGlnArgPheProSerLysGlyLysGly 340
 Db 1434 AGGRACCAAGGCAACCTTAATGAAAGAACGGTTCTCTAGTAAGGCCAAAGGT 1493
 Qy 341 LeuProIleProSerArgGlyLeuAspAsnGluIleLeuAsnGluMetAspSerProAsn 360
 Db 1494 CTCGCATTCCTCTGGCTGCTGATAATGATAATGAAATCTTAAT 1553
 Qy 361 GlyProSerHisGlnAsnIleLeuIleThrGlyArgLysTyrHistYrValProHisAsp 380
 Db 1554 GGCCCCAGTCATGAGAAATAAACTACATGGAGAAATAATCATATGACCCACAGA 1613
 Qy 381 GluAsnAsnSerThrArgAsnLysGlySerTrpGlyArgGln 400
 Db 1614 CAAATAATCTCACGGATAAAGGCTATGCCCCTAGCAA 1673
 Qy 401 ProIleSerAsnArgArgPheSerSerArgArgAspSerAsnSerGluSerAsp 420
 Db 1674 CCCCATTCACAGGAGGTATCTCCGTAGAAGGATGACATGAGTCACTGAC 1733
 Qy 421 SerGlySerSerGluSerAspGlyAsp 430
 Db 1734 AGTGCAGTCAGTGAAGGCGTGTGAC 1763
 RESULT 7
 US-09-794-422-3
 ; Sequence 3, Application US/09794422
 ; Publication No. US20030166239A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brown, Thomas A.
 ; De Wet, Jeffrey R.
 ; APPLICANT: Gowen, Lori C.
 ; APPLICANT: Hames, Lynn M.
 ; TITLE OF INVENTION: Mammalian Osteoregulins
 ; FILE REFERENCE: PC1045
 ; CURRENT APPLICATION NUMBER: US/09/794, 422
 ; PRIORITY APPLICATION NUMBER: 2001-02-27
 ; PRIORITY FILING DATE: 2001-02-27
 ; PRIORITY APPLICATION NUMBER: 60/1185, 617
 ; PRIORITY FILING DATE: 2000-02-29
 ; PRIORITY APPLICATION NUMBER: 60/234, 500
 ; PRIORITY FILING DATE: 2000-09-22
 ; NUMBER OF SEQ ID NOS: 46
 ; SOFTWARE: PatentIn ver. 2.0
 ; SEQ ID NO: 3
 ; LENGTH: 1682

; TYPE: DNA
; ORGANISM: Mus musculus
US-09-734-422-3

Alignment Scores:
Pred. No.: 1. 06e-86
Score: 983.50
Percent Similarity: 62.16%
Best Local Similarity: 50.47%
Query Match: 43.15%
DB: 12

US-09-700-696c-2 (1-430) x US-09-794-422-3 (1-1682)

Qy 6 SerileSerAsnlysGluAsnThrHisAsnGlyLeuArgMetSerIleTyrProLysser 25
Db 165 AGCTCGGCAATCAGACATTCAAGGACTTG2GATCTGTATCTGATCCC 225
Qy 26 ThrGlyAsnlysPheGluAspGlyAspAspAlaIleSerIleLeuAspGlnGlu 45
Db 226 ACGGTGGATAAGGACAAGGAGATGGCAAGGGTCTCTTACCCGGCTGCCAGAAC 285
Qy 46 GluTyrGlyAlaAlaLeuIleArgAsnAsnMrglnHisIleMetGlyProValThrAla 65
Db 286 AGGTATGGTGTGCTCCAGAAATACGCGCTGTAAGAGTCAGTGGACTGG 345
Qy 66 IleLeuGlyLeuGluAsnlysGluAsnThrProArgAsnValLeuAsnIleIle 85
Db 346 GCGGAACATCCGGAAACAGGGAAAGACCTCAGACTGTTAAGCGTTAAT 405
Qy 86 ProAlaserNetAspTyrAlaLysAlaHisSerIleAspIleSlysPheGlnIargAsp 105
Db 406 CCAGCAGATGTCAAATGATGCTAAACTCTCTTAAAGACATAAGAAGAGTTA 465
Qy 106 SerGlnAlaGlnIlySerProValIysSer-----LysSerThrIleArgIleGln 122
Db 466 CTGGTAACCCAGAGCCGGTCAAAGCAAAACACACCCAAACACCCGCAAGACCGA 525
Qy 123 HisAsnIleAspTyrIleUtyHisIleSerIlySerIleProSerAspPheGlu 142
Db 526 CGGAGGACTCACTTGACACATCCAGAACATCCAGAACAGACTCCCGTGACCTTGA 585
Qy 143 GlySerGlyTyrThrAspIleUtyGluArgGlyAspAsnAspIleSerProHeSerGly 162
Db 586 GGCAAGTGCTGCCAGATCTCTAGTGAAGGAGTATGATGTCGGCTCTGAGTGA 645
Qy 163 AspGlyGlnPropheAspIleProGlyLysGlyGluAla--ThrGlyProAspIle 181
Db 646 GATGGCAACATTTATGACATTCATCCGAAAGAGGGCTGGTGTCTGAA-- 702
Qy 182 GluGlyLysAspIleGlnThrGlyPheAlaGlyProSerIleAlaGluSerThrHisIle 201
Db 703 -----AGCTCAACTAGTGCSCCCCTCTAGGTCAAGCTGAAAGCTTATGACCA 756
Qy 202 AspThrLysSlysProGlyTyrAsnGluIleProGluArgGluGlyAsnThr 221
Db 757 CATATGAGTGGACTAGGCTTAATGAGATCCGGGAGAGGACATGTGGAGTGGCC 816
Qy 222 IleGlyThrArgAspGluThrAlaIleAspAlaValAspValIleLeuIleGlu 241
Db 817 TATGGCACACAGAACAGCTGCAAGGCGCAGCTGCACTGGAGCTGTCGGAG 876
Qy 242 GlySerAsnAspIleMetGlySerThrAsnPhelysGluLeuProGlyArgGluGlyAsn 261
Db 877 GCCAGGCTATGAAATCATCAGGCAACTCCGGAAACTCCGGAAAGAGGAAAC 936
Qy 262 ArgValAspAlaGlySerGlnAlaHisGlnGlyLysValGluPheIstTPropo 281
Db 937 AGAATTAATGCCGCAAGCAGCAAAATGTCATCAAGGAAAGTAGATTCACTATCCA 996
Qy 282 AlaProSerGlySerGlyAspIleGluSerSerAspAlaAlaGluSerThrAsnIle 301
Db 997 GTGGCCTGAGAGAAAGCTAAAGCTAAAGGGGGTGGAGCATGAGGAACTCAGGG 1053

Qy 302 AsnGluIleProLyssAsnGlyLeuGlySerThrArgLysGlyValAspHisSerAsnArg 321
Db 1054 AACGAAATCCCAGGGCAAGCTAGCTCAAGATGCCAAAGGG 1113

Qy 322 AsnGlnAlaIleLeuAsnGluIysGlnIysGlnIysGlySerIleGlyLeu 341
Db 1114 AACCAATTAACTTACGTTGACTGCAAGATTCCAGTTCAAGGAAAGCC 1173

Qy 342 ProIleProSerArgGlyLeuAspIleGluMetAspSerPheAsnGly 361
Db 1174 GCTCTGCCCTCTCAGCTCTAGTATGAGTAAAGTGA----- 1215

Qy 362 ProSerHisGluAsnIleIleThrHisGlyArgIysTyrHistYtyValProHisArgGln 381
Db 1216 -----GAAAC-----CATTAGTGTTCCAGTGACAA 1242

Qy 382 AsnAspSerThrArgAsnIysGlyMetProGlnGlyLysGlySerItp---GlyArgGln 400
Db 1243 AATAATCTTACACGGATAAAGGGATGTCACAGCAGAGGCTCTGGCCTTCGAGAAAGA 1302

Qy 401 ProHisSerAsnArgPhesSerAspSerGluSerSerAspIleThrAsp 420
Db 1303 CCCAAATCCCCACAGGGGGTAGCACCCGCCAAAGAA---GACAGCAAGCAGTCGTOATCC 1359

Qy 421 SerGlySerSerSerGluSerAspGlyAsp 430
Db 1360 ATGGGAGGTTCTAGTGAGTGTAGTGTGAC 1389

RESULT 8
US-09-794-422-1
; Sequence 1, Application US/09794422
; Publication No. US20030166229A1
; GENERAL INFORMATION:
; APPICANT: Brown, Thomas A.
; APPICANT: De Wet, Jeffrey R.
; APPICANT: Gowen, Lori C.
; APPICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins
; FILE REFERENCE: PC10445
; CURRENT APPLICATION NUMBER: US/09/794,422
; CURRENT FILING DATE: 2001-02-27
; PRIORITY APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIORITY APPLICATION NUMBER: 60/234,500
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1655
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-794-422-1

Alignment Scores:
Pred. No.: 2 6.6e-82
Score: 938.50
Percent Similarity: 59.95%
Best Local Similarity: 49.41%
Query Match: 41.18%
DB: 12
Length: 1655
Matches: 211
Conservative: 45
Mismatch: 146
Indels: 25
Gaps: 8

Qy 9 AsnIleGluAsnIleThrAsnGlyLeuArgMetSerIleTyrProIleSerThrGlyAsn 28
Db 146 AACAAAGCCAAATATCCTC-----TTAGCATCTGTAAGCCATGGGGGT 196

Qy 29 LysGlyPheGluAspGlyAspAspAlaIleSerIleLeuIleAspIleGluGluItyGly 48
Db 197 AATGGAAACAGGGTGGAGATGGCTCCCTTCAACCTGCTGTGACCAAGAGAACGGCGGGGT 256

Qy 49 AlaAlaIleIleArgAsnAsnMetGlnHisIleMetGlyProValThrAlaIleLeu 68

257	GCCACCTCCTCAAGAAATATCACTGCCCCCTAAAGAGTCCTGGTGCAGGGACTGAAGTA	316	Db	1289 CACCGGGGGTAAGCACCCGCCAAAGA--GACGTAGTCATCATCCAGTGGGAGT 1345
69	LeuGlyGluGluAsnLysGluAsnThrProArgAspValLeuAsnLeileProAlaser 88	Qy	424 SerSerGluSerAspGlyAsp 430	
317	CAGGAGCACGAAACAAAGGAAACCTAGAGGATAGCTAACATTGAAAGATAGAT 376	Db	1346 TCTAGGGAGAGGAGTGTTGAC 1366	
89	MetAsnTyraLalaHisSerLysAspLysLysProGlnArgProSerGlnAla 108	Qy	RESULT 9	
377	GTCACAATACTAACACTAGAGATAAGAGAAACCAACAGAGGATCTACTCTC 436	Db	US-10-363-798-1	
109	GlnLysSerProValLysSerSerThrHisArgLysGlnAsnL1AspTrpLeu 128	Qy	Sequence 1, Application US/10363798	
437	CAGACAGGCCAGGAAACAAACACACCCCCTGGGCCGAGAACGACACTCTA 496	Db	Publication No. US20030180280A1.	
129	LysHi-SleSerLysValLysLysProSerAspHeGluGlySerGlyTrpThrAsp 148	Qy	GENERAL INFORMATION:	
497	ACATATCTCCCTCAATCAAGAAAGATTCTAGGAGCTGGTCTCCAGAC 556	Db	APPLICANT: Kong, Xiangyu in	
149	LeuGlnGluArgGlyAspAsnAspSerProHeSerGlyAspGlyGlnProHeLys 168	Qy	APPLICANT: Xiao, Shangxi	
557	CTCTAGTAGGGGATATGAGCCTCTTCAAGGAGATGACACATTTATG 616	Db	APPLICANT: Zhao, Guoping	
169	AspIleProGlyLysGlyGluAlaThrGlyProAspLeuGlu-----GlyIysAsp 185	Qy	APPLICANT: Yu, Chuan.	
617	CACATCCGACAGGAGGTCTGGATCTGATCTGATCTGAAAGGCTCAGCTGGTCAACCT 676	Db	APPLICANT: Hu, Lanjuan	
186	IleGlnThr-GlyPheAlaGlyProSerGluAlaGluSerThrHisLeuAspThrLysLys 205	Qy	TITLE OF INVENTION: METHOD OF DIAGNOSING AND TREATING DENTINOPHENOMENON GENE AND CODED	
677	GTG-----TCAGCTCCGCAAATTGTCGAGTGTGACGACACAGATGGA 724	Db	TITLE OF INVENTION: TYPE II USING DENTIN SIALOPHOSPHOPROTEIN GENE AND PRODUCT THEREOF	
206	ProGlyTyrasngGluIleProGluArgGluGluAsnThrIleGlyThrArg 225	Qy	FILE REFERENCE: 95-E.7805W0	
725	CTGGCTCTTAATGGATTCAGGAGAGGTCACATGGGCTGCTATGAAACCGAGA 784	Db	CURRENT APPLICATION NUMBER: US/10/363-798	
226	AspGlutThrAlaLysGluAspValSerIleuValGluGlySetAspAsp 245	Qy	PRIOR APPLICATION NUMBER: CN 00125042.6	
785	GGAAAATCTGCGGGAGGGTTCGCGGATGAGGCTTGTGAGGGCAGGCTATGAA 844	Db	PRIOR FILING DATE: 2003-03-05	
246	IleMetGlySerSerAsnPhenylsclLeuProGlyArgGluGlyAsnArgValAspAla 265	Qy	NUMBER OF SEQ ID NOs: 44	
845	ATCAGGGGAGTACCAAATTAGGAGCTCCCTGAAAGAAACAGTCATGCC 904	Db	SOFTWARE: PatentIn version 3.1	
266	GlySerGlnAsnAlaHisGlnGlyLysValGluPheHistYProProSerLys 285	Qy	SEQ ID NO: 1	
905	AGCGGCCAAATGTCATCAAGGAAAGTAGAAATTCTACACCRAAGGCCCTCAA 964	Db	LENGTH: 8201	
286	GluLysArgLysGluGlySerSerAsnPhenylsclLeuProGlyArgGluGlyAsnArgValAspAla 265	Qy	ORGANISM: Homo sapiens	
965	GAGAAGGTTAAAGGGGAGCAGGGAGCACAGGGAGCTAACATGAATCCCC 1024	Db	US-10-363-798-1	
306	LysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsnArgGlnAlaThr 325	Qy	Alignment Scores:	
1025	ATGAGGCCAAAGGGTCCCGGCCAAAGGGCAAGGGCAGTCT-----TCT 1132	Db	Pred. No.: 0.000546	
326	LeuAsnGluLysGlnArgPheProSerLysGlySerThrArgLysGlyAsnThrHisArgLysGlyLeu-ArgMetSerIleTyprI 23	Qy	Score: 149.50	
1085	TTCAGCTGAAAGGCCAAAGGGTCCCGGCCAAAGGGCAAGGGCAGTCT-----TCT 1132	Db	Percent Similarity: 38.43%	
346	ArgGlyLeuAspAsnGluLysAsnGluMetAspSerHeAsnGlyProSerHisGlu 365	Qy	Best Local Similarity: 20.09%	
1133	CACAGTCCTGGTAAATGAGCTTAAGAGTGAAGAACACTCTCTAATGCTAGAGAG 1192	Db	Query Match: 6.52%	
366	AsnIle---IleThrHisGlyArgLysGlyThrIstYrValProHisArgGlnAsnAsnSar 384	Qy	DB: 12	
1193	GCGATTTGAATACACACAGGAGAACGCCAC-----CCT 1228	Db	Length: 8201	
385	ThrArgAsnLysGlyMetProGlnGlyLysGlySerTrp---GlyArgGlnProHisSer 403	Qy	Matches: 92	
1229	ACAGGAAATACGGGAGATCTACGGGGAGGCTCTGGCCMTCAGAGAACCCATCC 1288	Db	Conservative: 84	
404	AsnArgArgPheserSerArgArgAspAspSerSerGluSerSerGlySer 423	Qy	Mismatches: 218	
5616	CTCTGATGAA-----	Db	Indels: 64	
5616	CTCTGATGAA-----	Db	Gaps: 14	
5616	CTCTGATGAA-----	Db	US-09-700-696-C-2 (1-430) x US-10-363-798-1 (1-8201)	
5214	AAATATTCACTGTTAATCTTCTCCATCTCTCCATAGGAAATTGAAATCAAGGG 5273	Qy	4 GlutYrSerIleSerAsnLysGluAsnThrHisAsnGlyLeu-ArgMetSerIleTyprI 23	
5214	AAATATTCACTGTTAATCTTCTCCATCTCTCCATAGGAAATTGAAATCAAGGG 5273	Db	5214 AAATATTCACTGTTAATCTTCTCCATCTCTCCATAGGAAATTGAAATCAAGGG 5273	
23	oLysSerThrGlyAsnLysGlyPhe----GluAspGlyAspAspAlaIleSerLysIe 41	Qy	5214 AAATATTCACTGTTAATCTTCTCCATCTCTCCATAGGAAATTGAAATCAAGGG 5273	
5274	TCCAGGAGTGGCCAACACAAATTACCAAGAAAGAGTGGTGGCAAAGGCAACGAGTAA 5331	Db	5274 TCCAGGAGTGGCCAACACAAATTACCAAGAAAGAGTGGTGGCAAAGGCAACGAGTAA 5331	
41	uHisAspGlnGluGluLysGlyIgYalaAlaIleIleArgAsnAsnMetGlnHisIleMetG1 61	Qy	5274 TCCAGGAGTGGCCAACACAAATTACCAAGAAAGAGTGGTGGCAAAGGCAACGAGTAA 5331	
5332	-GAGGATAAAAGGACACACATGGATGATGCTGAACTGCTGAAAGGCAACGAGTAA 5387	Db	5332 -GAGGATAAAAGGACACACATGGATGATGCTGAACTGCTGAAAGGCAACGAGTAA 5387	
5332	yProValThrAlaIleLysLeuIleGlyGluGluAsnLysGluAsnThrProArgAsnV 81	Qy	5332 -GAGGATAAAAGGACACACATGGATGATGCTGAACTGCTGAAAGGCAACGAGTAA 5387	
5388	AGAGGTGTCACATAGGAACTAGAAGGACCTGCTGAACTGCTGAAAGGCAACGAGTAA 5438	Db	5388 AGAGGTGTCACATAGGAACTAGAAGGACCTGCTGAACTGCTGAAAGGCAACGAGTAA 5438	
81	Ileu-----	Qy	5388 AGAGGTGTCACATAGGAACTAGAAGGACCTGCTGAACTGCTGAAAGGCAACGAGTAA 5438	
5439	AGTTGGACACACCAATACTGGTGTGACGCAATAATGCTGATGATGCACTGATGATT 5498	Db	5439 AGTTGGACACACCAATACTGGTGTGACGCAATAATGCTGATGATGCACTGATGATT 5498	
84	elleProAlaSerMetAsnTyraLalysValIleSerLysAspProGlnAr 104	Qy	5439 AGTTGGACACACCAATACTGGTGTGACGCAATAATGCTGATGATGCACTGATGATT 5498	
5499	TGATGATAAGTCCTGACAGGAGATGATCCAAATAGCAGTGTGAACTGCAATGCAATG 5558	Db	5499 TGATGATAAGTCCTGACAGGAGATGATCCAAATAGCAGTGTGAACTGCAATGCAATG 5558	
104	GaspSerGlnAlaGlnLysSerProValLysSerProThrHisArgIleGlnHisA 124	Qy	5499 TGATGATAAGTCCTGACAGGAGATGATCCAAATAGCAGTGTGAACTGCAATGCAATG 5558	
5559	TGATGTTAAATCAGAA-----	Db	5559 TGATGTTAAATCAGAA-----	
124	nileAspTyrIleLysHisIleSerLysValLysIleProSerAspPheGluGly 144	Qy	5559 TGATGTTAAATCAGAA-----	
5616	CTCTGATGAA-----	Db	5616 CTCTGATGAA-----	

Qy 203 ThrlsLysProGlyTyrAsnGlutleProGluArgGluAsnGlyGlyAsnThrIle 222
 Db 2065 -----GGAGAGTTTTTCATCAAGGCAATGCAGGGACAGAGGA 2106
 Qy 2223 GlyThrArgAspGluThr-----AlaLysGlu 231
 Db 2107 GGACAGACAGACAAACTGACAGCACAGGAGGACAGCTTCCTAAGTAGAAGAG 2166
 Qy 232 AlaAspAlaValAspValSerLeuValGluGlySerAspIleMetGlySerThrAsn 251
 Db 2167 GATGATTATCCCTCTGAAAGACTATAGAGCATGAAACCGCTATAATGCCAAACGGCT 2226
 Qy 252 PheLysGluIleProGlyArgGluGlyAsnGlySerGln----- 268
 Db 22227 AAAGAAAAAAACCCGGAAATCAGGCAGGCAAGTTGTGTTAACCTGAAAGTCCCTGAC 2286
 Qy 269 AsnAlaHisGlnGlyLysValGluPheHistYrProProLaproSerLysGluLysArg 288
 Db 2287 AGAGCAGTTAGGGACCATCAT-----CCAGATCCGAAATTGAGAAAGC 2334
 Qy 289 LysGluGlySerSerAspAlaAlaGluSerThrAsnTyrAsnGluIleProLysAsnGly 308
 Db 2335 AAGCARGAAACTAGATGATTGTGATAAGTGTGAAAACAGTGAG----- 2379
 Qy 309 LysGlySerThrArgGlyGlyValAspHiSerAsnArgAsnGlnAlaThrLeuAsnGlu 328
 Db 2380 -----ACTGTGCCAAAGGGTCAACACAGGGCAGGAAACCAAATCAATGTTGGAA 2433
 Qy 329 LysGlnArg-----PheProSerLysGlyLysSer 338
 Db 2434 AAAGAACGCCCTCTGGCAGATAAGAACAGAGCACATTGAAACGAGTGTATTCT 2493
 Qy 339 GlnglyLeuProSerArgGlyLeuAspSerGlnLysAsnGluMetAspSer 358
 Db 2494 GACGGCATAAAATTCAAGACTCCGAAATTAAGGTGAAGTGTTCGAATAAGATCTGAT 2553
 Qy 359 Phe-----AsnGlyProSerHisGluAsnIleThrHisGlyArgLysTyrHistYr 376
 Db 2554 TATCTGAAGAACGAAACCTGAGAACATCTGAGACCTCAGGSCCT----- 2601
 Qy 397 TrpGlyArgAsnProHisSerAspArgAsnSerThrArgAsnLysGlyMetProGlnLysLysGlySer 396
 Db 2602 -----GCAGGGGAGGCTGAGGAGAACCTGAGAACCTCAGGSCCT----- 2628
 Qy 277 ValProHisArgGlnProHisSerAspArgPheserSerArgAspSerSer 416
 Db 2629 -----AAGAGGACCATGAGAAC-----ACAGAGAAGTACATGGCACA 2667
 Qy 417 GluSerSerAspSerGlySerSerGluUserAsp 428
 Db 2668 GAAAGCCAGGGGCTGCTGCAACCTGAAAGAT 2703

RESULT 11
 US-09-785-770A-14
 Sequence 14, Application US/09/785770A
 Patent No. US20020103360A1
 GENERAL INFORMATION:
 APPLICANT: Pan, Yang
 INVENTOR: Barnes, Thomas M.
 TITLE OF INVENTION: A NOVEL PROTEIN RELATED TO MELANOMA-INHIBITING PROTEIN
 FILE REFERENCE: 07334-320001
 CURRENT APPLICATION NUMBER: US/09/785,770A
 CURRENT FILING DATE: 2001-02-16
 PRIOR APPLICATION NUMBER: US 09/387,462
 PRIOR FILING DATE: 1999-09-01
 PRIOR APPLICATION NUMBER: US 09/145,056
 PRIOR FILING DATE: 1998-09-01
 NUMBER OF SEQ ID NOS: 24
 SOFTWARE: PatentIn Ver. 4.0
 SEQ ID NO 14
 LENGTH: 8121
 TYPE: DNA

ORGANISM: Homo sapiens
 FEATURE: 5' UTR
 NAME/KEY: (1)...(4)
 LOCATION: (1)...(4)
 NAME/KEY: CDS
 LOCATION: (5)...(5725)
 NAME/KEY: 3' UTR
 LOCATION: (5726)...(8121)
 US-09-785-770A-14

Alignment Scores:
 Pred. No.: 0.000603 Length: 8121
 Score: 148.000 Matches: 106
 Percent Similarity: 34.7% Conservative: 65
 Best Local Similarity: 21.5%
 Query Match: 6.49%; Indels: 112
 DB: 10 Gaps: 24

US-09-700-696C-2 (1-430) x US-09-785-770A-14 (1-8121)

Qy 1 ValAlnLysGluTyrSerIleSerAsnLys-----GluAsnThrHisAsnGly 16
 Db 1376 GTAAACGCAAGAACATCACATTAAGGAAAGGGAGGGAGTTCAAGAATCCAAGGGGGC 1435
 Qy 17 Leu-----ArgMetSerIleTyrPro 23
 Db 1436 CTGGTACAAGATGAGCACGATTAGAGGTAAATCAAGAAGGGCATGTCGACAGT 1495
 Qy 24 LysSerThrGlyAsnLys-----GlyPheGluAspGlyAspAspAlaIle 38
 Db 1496 TCTGTGTCAAGCAATAACCTCAACTCTATGCCAGGTGCTGCTGAAACGGTAAAGACATTA 1555
 Qy 39 SerLysLeuHisArgPglnglugu-----TyrglyalaalaLeu--IleArgAsn 54
 Db 1556 AAATCAGCTTATGATGATACGAAAATGACCTAAAGGGCAGTATTCTATCTCAA 1615
 Qy 55 AsnNetGlnHisIleMetGlyProValThrAlaIleLeuLeuGlyLysGluAsnLys 74
 Db 1616 GGAATGCTTCACGAAAGAAAGCTGTGAGGAGCAGTATTGAAAGTTGGCTCAAGATGTAA 1675
 Qy 75 -----GluAsnThrProArgAsnValLeuAsn-----IleIleProAlaSerMet 89
 Db 1676 TCCTCAGAAAAGCTGCAGGAAATCAATGAAATGAACTGAAAGGATCCCTG 1735
 Qy 90 AsnTyrAlaLysAlaHisserLysAspLysLysProGlnArgAspSerGlnAlaGln 109
 Db 1736 GGTAGTGCACCATCTGGGAGATGACCCCTAAACGCTTAAGCAGTGTGGAGGAA 1795
 Qy 110 LysSerProValLysSerIleAspTyr 127
 Db 1796 GACCCCTTGATAATGGGCCAAACTGACACGCTTCAGTGGAGCATCAACGTGAGGA 1855
 Qy 128 LeuIlysHis-----LeuSerIlysValLeuSerAspPheGluGlySergly 145
 Db 1856 TTGAAAGGAAATAGTGTCTTAAACTAAACCAACCTAGA --TTTCNCCTCTCAGAT 1912
 Qy 146 TyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspGlyGln 165
 Db 1913 GAGATGATTGCTGCCAGAACATGGAAAGAGCAGCTTCCCATTCTGGAAAGAAATCT 1969
 Qy 166 ProPhe-----LysAspIleProGlyLysGlyGluIalnrglyProAspLeuGlu 182
 Db 1970 CCCCTGGCAACAGAAAGAGATGTC-----GCTGCCACAGGCCAGTAAGCAAGGACTCCTGCTGAT 2017
 Qy 183 GlyLysAspIleGlnThrGlyPheAlaIleProSerGluAlaGluSerThrHisLeuAsp 202
 Db 2018 AGTGAGAGAGATANG-----CTCTCTGAGGGAGCAAGGAGCTCTGCTGAT 2068
 Qy 203 ThrLysLysProGlyTyrAsnGlnIleProGluArgGluIasnGlyGlyAsnThrIle 222
 Db 2069 -----GAAGATTTTTTCATCACAGGGCAATGAGGGCACAGGGTAA 2110
 Qy 223 GlyThrArgAspGluThr-----AlaLysGlu 231

1 SOFTWARE: PatentIn Ver. 2.0
2 SEQ ID NO: 301
3 LENGTH: 2673
4 TYPE: DNA
5 ORGANISM: Homo sapiens
6 FEATURE:
7 NAME/KEY: CDS
8 LOCATION: (33) .. (2348)
9 US-10-153-668-301

10 Alignment Scores:
11 Pred. No.: 0.000862 Length: 2673
12 Score: 140.00 Matches: 87
13 Percent Similarity: 32.08% Conservative: 49
14 Best Local Similarity: 20.52% Mismatches: 144
15 Query Match: 6.14% Indels: 144
16 DB: 14 Gaps: 17

17 US-09-700-696C-2 (1-430) x US-10-153-668-301 (1-2673)

18 Qy 23 ProLysserThrGlyAsnLysGlyProGluAspGlyAspSerLysLeuHis 42
19 Db 660 CCTGGAAAGGCCACGCAATGCCTTCAGGACAGACTGGCCAGGAAAGCAC 719

20 Qy 43 AspGlnGluGlutYrgIyAlaAlaLeuIleArgAsnAsnMetGlnHisIleMetGlyPro 62
21 Db 720 CTGGGTGAACCCATGGAAAGGGTGTGAGTCAAACAAAGGRGAC----- 767

22 Qy 63 ValThrAlaLileLysLeuLeuGlyGluAsnLysGluAsnThrProArgAsnValLeu 82
23 Db 767 -----
24 Qy 83 AsnIleIleProAlaSerMetAsnTyrrAlaLysSerProValLysLysPro 102
25 Db 768 -----
26 Qy 103 GlnArgAspSerGlnAlaGlnLysSerProValLysSerThrHisArgIleGln 122
27 Db 798 GATGCCAAGAGTGATGAGAACGCTGTCGGTGGACAGAGAAATCACAC----- 848
28 Qy 123 HisAsnIleAspTyrIleLysLysLeuSerLysValLysLysIleProSerAspGlu 142
29 Db 849 -----
30 Qy 143 GlySerGlyTyrThrAspLengLgiuArgGlyAspSerProPheSerGly 162
31 Db 864 -----
32 Qy 163 AspGlyGlnProPhelysAspIleProGlyIysGlyGluAlaThrGlyProAspLeuGlu 182
33 Db 891 GACAATGCAAGGGAGAACCG-----CCCTCTAGTGCCGCTAAAGAAGGAGAG 947

34 Qy 183 GlyLysAspIleGlnThrGlyPheAlaLysProSerGluAlaLysUser---ThrHisLeu 201
35 Db 948 GGCAAGGCTGAAGAGAGACTGTGCTCCCTGAGGGCTTAGACAAACCTG 1007

36 Qy 202 AspThrLysLysProDltyAsnGlyIleProGluArgGluAsnGlyGlyAsnThr 221
37 Db 1008 -----
38 Qy 242 GlySerAsnAspIleMet-----
39 Db 1089 GGAGCAAGGAGACCCTGCCCCAAGGTTCAACACCTAAAGACTCCA 1148
40 Qy 256 ProGlyArgGluGlyAsnArgValAspAlaGlySerGlnAlaHisGlnGlyLysVal 275
41 Db 1149 GAAAGGAAAGTCAAACATATTGAGTAGAAAGTCCTGAGCTGCTG 1205
42 NUMBER OF SEQ ID NOS: 488

Db	1206 GAGGAGACAGATATGGAGATGAATTGAGCAGGCCAACCATGTCTTGAATCCTACCTC 1265	Qy	23 ProlySerThrGlyAsnLysGlyPheGluAspGlyAspAspAlaIleSerLysLeuHis 42
Qy	281 -----ProAlaProSerAspGlyAspGlySerGluLeuSerAspAlaAlaGluSer 298	Db	663 CCTGGAAAGGCCAACGCCAATGCCCTTCAGCACAGACTCGGGCCAGCAAGAAGGACAC 722
Db	1266 AGCTATGACCAGGCCGGAGANAGAAAAGTTGAAACT---TGAGCCACGGCA 1322	Qy	43 AspGlnGluLeuGlyAlaAlaLeuLeuArgAsnAsnMetGlnHistileMetIlePro 62
Qy	299 ThrasntryAsnGluIleProLyAspGlySerThrArgLySlyValAspHis 318	Db	723 CTGGGTGAACCCATGGAAAGGGTTTGAGTCACAAACAGGACAC----- 770
Db	1323 CTTGAGATAAGGACTTAATAATGACTCTAAAGGACTGGTA 1382	Qy	63 ValThrAlaLileSleLeuGlyGluGluAsnLysGluAsnThrProArgAsnValLeu 82
Qy	319 SerAsnArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLyGlyLySSer 338	Db	770 ----- 770
Db	1383 GTTCAAGATTACCCAAAGGTGAAACAACAAAGTCAGAGAAAGCCGCTGAGCTGATTTA 1442	Qy	83 AsnLileProAlaSerMetAsnTyraLysAlaHisSerLysAspLysLysPro 102
Qy	339 GlngLyLeu----- 341	Db	771 -----AAATCTCCACACAGGACAAACGCCGTRG 800
Db	1443 GCCAAGCTGTAGAAAGGTGCGTGTGCGCACTGTCAGACCTCCCGTACCCGGC 1502	Qy	103 GlnArgAspSerGlnAlaGlnLysSerProValLysSerThrHisArgLleGln 122
Qy	3442 -----ProIleProSerArgGlyLeuAspAsnGluIleLysAsnGlu 355	Db	801 GATGCCCAAGAGTGTAGAGAAGGGCTCTGNGTGAACAGAGAAATAACAC----- 851
Db	1503 ATACAGGCCATTACCCGTTGCACTGCTCAGCTCATATATCTCTCCAGCAAG 1562	Qy	123 HisAsnIleAspIleLeuLysHisLeuSerLysValLysIleProSerAspPheGlu 142
Qy	3556 MetAspSerPheAsnGlyProSerHisGluAsn----- 366	Db	852 -----AAGGCCCTCTCAA----- 866
Db	1563 CGAAAAGGCTCTCITCACCCAGAAAGAGAAAGAGAAAG 1622	Qy	143 GlySerGlyTyrThrAspIleGlnGluArgGlyAspAsnAspIleSerProPheSerGly 162
Qy	367 -----IleIleThrHisGlyArgLysTyrHistItyValPro----- 378	Db	867 -----GAGGAAACCCAGGGCACCCCTAGGG 893
Db	1623 AATTCAAAGATGCACTGTTCTCGCTTCCAAGTGTGCCTATCTCCCTAAATGATGAC 1682	Qy	163 AspGlyGlnProPheLysAspIleProGlyLysGlyGluIalThrGlyProAspLeuGlu 182
Qy	379 ---HisArgLln 381	Db	894 GACAATGCCAGGGAAACCG---CCCTCTAGGGCTAAAGAGAAAGGAGAGAGAG 950
Db	1681 TTGACCAACCAA 1694	Qy	183 GlyIysAspIleGlnThrGlyPheAlaGlyProIleGluAsnUser---ThrHisLeu 201
<hr/>			
RESULT 13	US 10-101-510-398	Qy	202 AspThrIlysProGlyLysProGluArgGluGluAsnGlyGlyAsnThr 221
Sequence 398, Application US/10101510			
; Sequence 398, Application US/10101510			
; Publication No. US20030148295A1			
; GENERAL INFORMATION:			
; APPLICANT: WAN, JACKSON			
; APPLICANT: WANG, YIXIN			
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE			
; FILE REFERENCE: 15117.0012			
; CURRENT APPLICATION NUMBER: US/10/101,510			
; CURRENT FILING DATE: 2002-03-20			
; PRIORITY APPLICATION NUMBER: 60/176,947			
; PRIOR FILING DATE: 2001-03-20			
; NUMBER OF SEQ ID NOs: 805			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO: 398			
; LENGTH: 4839			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE: GluPhiHistYrPro			
; NAME/KEY: modified_base			
; LOCATION: (3080)..(73102)			
; OTHER INFORMATION: a, t, c, g, other or unknown			
; FEATURE: ProAlaProSerLysGluLysArgLysSerAspAlaIleGluSer			
; NAME/KEY: modified_base			
; LOCATION: (428)			
; OTHER INFORMATION: a, t, c, g, other or unknown			
US-10-101-510-398			
Alignment Scores:			
Pred. No.:	0.00187	Length:	4839
Score:	140.00	Matches:	87
Percent Similarity:	32.08%	Conservative:	49
Best Local Similarity:	20.52%	Mismatches:	144
Query Match:	6.14%	Indels:	144
DB:	12	Gaps:	17
US-09-700-696c-2 (1-430) x US-10-101-510-398 (1-4839)			
<hr/>			
Db	1446 GCCAAGCTGAGAAAGGTGCGTGTGAGCTGAGACTCCGTTACCGCG 1505	Qy	319 SerAsnArgAsnGlnAlaThrIleAsnGluLysGlnArgPheProSerLysGlyLySSer 338
Db	1386 GTTCAGAAATTACCAAGGTGAAACAAACGAGTCAGAGAAACCCGGTGGACTGTGATTAA 1445	Qy	339 GlnGlyIeu----- 341

3442 -----ProIleProSerArgGlyLeuAspAsnGluIleLysAsnGlu 355
 Qy :-----[:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 15056 ATACAGGCCAATTACCGTCACTGCCTCCTCGAGCTATATCTCCAGCAANG 1565
 Qy 3556 MetAspSerPheAsnGlyproSerHisGluAsn----- 366
 Db 1565 CGAAAAGGGTGTCTTCATCCCAGGAAGAGAAAGCTGAGAATG 1625
 Qy 3677 -----IleIleThrHisGlyArgLysTyrHistYrValPro----- 378
 Db 1626 AATTCCAATGATGAGGTGATTCTCGTTCAAAGTGCCATCTCCCTAAATGATGACC 1685
 Qy 3799 --HisArgGln 381
 Db 1686 TTGACCACCAA 1697

RESULT 14
 US-10-161-572-6
 Sequence 6, Application US/10161572
 Publication No. US20030087266A1
 GENERAL INFORMATION:
 APPLICANT: EXELIXIS, INC.
 TITLE OF INVENTION: IGS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
 CURRENT APPLICATION NUMBER: US/10/161,572
 PRIOR FILING DATE: 2001-06-05
 PRIOR APPLICATION NUMBER: US 60/296,076
 PRIOR FILING DATE: 2001-06-05
 PRIOR APPLICATION NUMBER: US 60/328,605
 PRIOR FILING DATE: 2001-10-10
 PRIOR APPLICATION NUMBER: US 60/338,733
 PRIOR FILING DATE: 2001-10-22
 PRIOR APPLICATION NUMBER: US 60/357,253
 PRIOR FILING DATE: 2002-02-15
 PRIOR FILING DATE: 2002-02-15
 NUMBER OF SEQ ID NOs: 63
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 6
 LENGTH: 1594
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-161-572-6

Alignment Scores:
 Pred. No.: 0 0.0314 Length: 35465
 Score: 133.00 Matches: 105
 Percent Similarity: 37.87% Conservative: 48
 Best Local Similarity: 25.99% Mismatches: 162
 Query Match: 6.10% Indels: 93
 DB: 14 17 Glys 17

US-09-700-696C-2 (1-430) × US-10-161-572-6 (1-35465)
 Qy 74 LysGluAsnThrProArgAsnValLeuAsnIleProAlaSerMetAsnTyrAlaLys 93
 Db 881 AAACAGGGACATCGGTAACTCTAGTC--ATGAGCCCAAAGTCCACCAA 937
 Qy 94 AlaHisSerLysAspLysLysLysProAlaArgSerGlnAlaGlnLysSerProAla 113
 Db 938 TCCACCACTACAAAAAGGCCCTTCATAACCGCCCAAGCAGGTCCCGAG 996
 Qy 114 LysSerLysSerThrHisArgLleGlnHisAsnIleAspTyrLeuIshisLeuSerLys 133
 Db 997 CAAAGCAGAACCCCCAGGGTGGAC-----CCACAGGACAG 1041
 Qy 134 ValLysLysIleProSerAspPheGluLysSerGlyLeuIshisLeuSerLys 153
 Db 1042 -----[:::|||||:|||||:|||||:|||||:|||||:|||||:
 Qy 174 GlyGluAla-----ThrGlyProAspLeuGluGlyLysAspIle 186
 Db 1119 GGCGAGGCCAGCTCCAAGAGGTGACCCAGCAGGCCAGCAACTCT-GCCAGG---ATA 1174
 Qy 187 GlutnGlypheAlaGlyProSerIuaAlaGluSerThrHisLeuAspThr----- 203
 Db 1175 AGAACTCATGGTGCAGACGGCTGGCCAGQGGTGAAGAACTCCACTTCACAGCAA 1234
 Qy 204 -----LysysProGlyTyrAsnGluIleProGluIargGluGluAsn----- 217
 Db 1235 AAAGGAGGCGGGAGAGGTTACGGCCGGCTAGAACAGCAACAGCAACAGCA 1294
 Qy 218 -----[:::|||||:|||||:|||||:|||||:
 Db 1295 AGCCAGCCPTAGAAATCTGAGCAAGAGAATTAACGCCACCCAGGGCTAGGTATAGGG 1354
 Qy 224 ThrArgAspGlu-----ThralalyGluAlaAspAlaValAspVal 237
 Db 1355 AGGAGTTCCGAGCTGGCTGAACTCCAGTACAGTCAAAGTCAGCAAGTCAACTGQAATT 1414
 Qy 238 SerIeuValGluGlySerAsnAspIleMetGlySerAsnPhenylSGLu----- 254
 Db 1415 CCCCTCAAGAGAGAGAGTCACAACCCATCTCCATCATCAAGGAGGTGAAGGTAC 1474
 Qy 255 -----LeuProDlyArgGlu-----GlyAsnArg 262
 Db 1475 GTGTGATGATCATCCCAGTAGGGAAAGAGTTAACGCCACTGAATGTCCAGCAGG 1534
 Qy 263 ValAspAlaGlySerGlnAsnAlaLahisGlnGlyLysValGluPheHistYrProPro--- 281
 Db 1535 GTCAAGAGTTATAACAGGCCAGGAGGCCAAAGTCACMG-CCATCTAG 1593
 Qy 282 AlaProSerLysGluIleGluGlySerSerAspAla-----AlaGluSerThr 299
 Db 1594 AAGGCCACAGAGTCAGAGTGGCAAGTCAGAGGAGCACAGCAGTCAGAAGTCA 1653
 Qy 300 AsnTyrAsnGluIleProLysAsnGlyLysGlySer-ThrArgLysGlyValAspHisse 319
 Db 1654 CAGTGGAGAGAAACCATAGCAGGCCAGAAGTCGCACCCGGAAAGGAAATT----- 1705
 Qy 319 IleSerArgAsnGlnIalathLeuAsnGluLysGlnArgpheProserLysSerGln 339
 Db 1706 ---CTGAGCCGAGATGGAAAGACAGCCCOAGTCTGAGGCCACRGCAAGGGAAAGTCA 1761
 Qy 339 nGlyLeuPro---IleProSerArgIleGlyLeuAspAsnGluIleSerAsnGluIleSerAsnGluNetAspSe 358
 Db 1762 AACCAATCTAGACCCCCAGAAGGAGAAACTCACACTGTCT----- 1807
 Qy 358 rPheAsnGlyProSerHisGluAsnIleIleThrHisGlyArgLysTyrHistYrVal - 377
 Db 1808 ---AGAACCCCCAGAAGAAGTCAGCATAGCCATTCCAGAAGCTCAGCAAAGAG 1863
 Qy 378 -ProHisArgGlnAsnAsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySerTr 397
 Db 1864 AGATCACAGGGGATCTACGCCCAAGGAGGTGGTCAGTCATCAGGAAGGCC 1923
 Qy 397 PglYArgGln---ProHisSerAsnArgGlyProSerSerArgArgTgAspSerSe 416
 Db 1924 CAACAGGAGAGATCAGGCCATCTAGAAGTCCACACAAGGAGATCGAGCG 1983
 Qy 416 rGluSerSer 419
 Db 1984 ATCTAGAGT 1993

RESULT 15
 US-10-161-572-8
 Sequence 8, Application US/10161572
 Publication No. US20030087266A1
 GENERAL INFORMATION:
 APPLICANT: EXELIXIS, INC.
 TITLE OF INVENTION: IGS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
 FILE REFERENCE: EX02-097C-PC

CURRENT APPLICATION NUMBER: US/10/161,572
 CURRENT FILING DATE: 2002-06-03
 PRIORITY NUMBER: US 65/296,076
 PRIOR FILING DATE: 2001-06-05
 PRIOR APPLICATION NUMBER: US 60/328,605
 PRIOR FILING DATE: 2001-10-10
 PRIOR APPLICATION NUMBER: US 60/338,733
 PRIOR FILING DATE: 2001-10-22
 PRIOR APPLICATION NUMBER: US 60/357,253
 PRIOR FILING DATE: 2002-02-15
 PRIOR APPLICATION NUMBER: US 60/357,600
 PRIOR FILING DATE: 2002-02-15
 PRIOR FILING DATE: 2002-02-15
 NUMBER OF SEQ ID NOS: 63
 SEQ ID NO: 8
 LENGTH: 36991
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-161-572-8

Alignment Scores:
 Prev. No.: 0.0332 Length: 36991
 Score: 139.00 Matches: 105
 Percent Similarity: 37.87% Conservative: 48
 Best Local Similarity: 25.99% Mismatches: 162
 Query Match: 6.10% Indels: 93
 DB: 14 Datascore: 14 Gaps: 17

US-09-700-696c-2 (1-430) × US-10-161-572-8 (1-36991)

Qy 74 LysGluAsnThrProArgAspValLeuAsnIleProAlaSerMetAsnTyAlaTyr 93
 Db 881 AAACCAGCAGCATCCGTAACTCGTCAGTCAGTCCAAAGTCACCCAA 937

Qy 94 AlaHisSerLysAspLysProGlnArgAspSerGlnAlaGlnIleSerProVal 113
 Db 938 TGACCAAGTACAAAAGGCCCTTCTAACGGCCAGGCAAGTCGCG 996

Qy 114 LysSerIleSerThrHisArgIleGinHisAsnIleAspTyrIleLysIleSerIys 133
 Db 997 CAAAGCAGAAACCCGAGGGTGACAC-----CGAACCAGGCCAG 1041

Qy 134 ValLysIleProSerAspPheGluGlySerGlyTyrThrAspLeuGlnGluArgIly 153
 Db 1042 -----CAAAAGCAGCAAGGCCAG 1059

Qy 154 AspAsnAspIleSerProPhsSerGlyAspGlyGlnProPhsIleProGlyIys 173
 Db 1060 CGACGTGAGATGCCACTAGCGGAGGCACACACGCCGCTGACACTG-GCAGBA 1118

Qy 174 GLYGLIAla-----ThrGlyProAspLeuGluGlyAspIle 186
 Db 1119 GGGAAACCAGCGAGGTCAAAGGGTCACCCAGGGCCAGGACTCT-GGCAGG--ATA 1174

Qy 187 GlnThrGlyPheAlaGlyProSerGluAlaIleSerThrHisLeuAspThr 203
 Db 1175 AGAACTATGGTCCAGCACGGCATGCCAGGGTGAAGACTCCACTTCAGGCA 1234

Qy 204 -----LysLysProGlyTyrAsnGluIleProGluArgGluAsn--- 217
 Db 1235 AAAGGGAGCGGGAAAGAGTACGGCGGCTAGACCAAGGGAAAGGGATGAC 1294

Qy 218 -----GlyGlyAsnThrIleGly 223
 Db 1235 AGCAGCCTAGAAATCTGAGCAAGAGTACCGGCCACAGGTACGGCTAGGATAGCG 1354

Qy 224 ThrArgAspGlu-----ThrAlaLysGluIleAspAlaValAspVal 237
 Db 1355 AGGAGTTCGAGCTGGCTGAACTCCAGTACGCCAAGCTCAAAACCCGACTGGAAATT 1414

Qy 238 SerLeuIleGlySerAsnAspIleMetGlySerAsnPhenylsGlu----- 254
 Db 1415 CCCCTCCAAAGGAAAGAGTGAACCCATCTCCATCAAGGAAAGGTGAAGCTAC 1474

255 -----LeuProGlyArgGlu-----GlyAsnArg 262
 Db 1475 GGTCAGATGATGATCATCCCCAGTAGGGAAAGGTTACAGGCCACTGAAAGTCAGCAGG 1534

Qy 263 ValAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHistyrProPro--- 281
 Db 1535 GTCAAAGGTTATAACGGCCAGCACCCGAGCAAGTCAG-CCAATCTAG 1593

Qy 282 AlaProSerLysGluIysArgLysGluGlySerSerAspAla-----AlaGluSerThr 299
 Db 1594 AACCCCGAGAAAGTCGAGAATGGCTGAGACAGGACGGERCAAGGAGTCAGAGTCAG 1653

Qy 300 AsnTyzAsnGluIleProLysAsnGlyLysGlySer-ThrArgLysGlyValAspIse 319
 Db 1654 CAGTTGGAGAGAAACCATAGGAGGCCAAAGAAGTCCACCCGAAACGGAATT----- 1705

Qy 319 rAsnArgAsnGlnAlaIleThrLeuAsnGlyLysGlnArgLysGlySerGly 339
 Db 1706 ---CTGAGCCAGATGGAAAGAACAGCCAGTCAGAAAGCCACAGAAAGGGAAAGTCA 1761

Qy 339 nGlyLysPro---IleProSerArgGlyLeuAspIleGluLysAsnGluMetAspSe 358
 Db 1762 AACCAAATCTAGAACCCCAGAGAGGAGGAGACTGCAACTGGCT----- 1807

Qy 358 rPheAsnGlyProSerHisGluAsnIleIleThrHisGlyArgLysTyrHistyrVal--- 377

Db 1808 ---AGAACCCAGGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1863

Qy 378 -ProHisArgGlnAsnAsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySerTr 397
 Db 1864 AGATCACAGGGGATCTAGCAGCCGCCAGGAGATGGTGCAGTCATGGAGGCC 1923

Qy 397 pGlyArgGln---ProHisSerAsnArgArgPheSerSerArgAsnGlyAspPheSer 416
 Db 1924 CRACAGGAGGAGTCACAGCGCATCTAGAAGTCCAAACAGGGAGAGATGCCGCCG 1983

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